

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: June 14, 2004, 14:40:51 ; Search time 21.4538 Seconds
(without alignments)
1838.444 Million cell updates/sec

Title: US-10-069-427-6
Perfect score: 755
Sequence: 1 PRYKKNKVELSLGLANLC.....REIWAECYKLVPRILPVYV 140

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1158786 seqs, 281726120 residues

Total number of hits satisfying chosen parameters: 1158786

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	728	96.4	372	12	US-10-425-114-66797
2	602	79.7	368	8	US-08-879-337-2
3	431	57.1	90	12	US-10-424-599-275960
4	384.5	50.9	454	12	US-10-425-114-58147
5	366	48.5	418	16	US-10-648-593-252
6	347.5	46.0	426	9	US-09-817-774-22
7	347.5	46.0	615	8	US-08-879-337-9
8	341.5	45.2	424	9	US-08-879-337-5
9	341.5	45.2	424	9	US-09-817-774-25
10	341.5	45.2	424	15	US-10-369-493-22601
11	311.5	43.9	427	9	US-09-817-774-23
12	319.5	42.3	475	9	US-09-729-674-142
13	319.5	42.3	475	9	US-09-817-774-26
14	319.5	42.3	475	16	US-10-429-160-32
15	317.5	42.1	471	9	US-09-817-774-27

16	300.5	39.8	637	8	US-08-879-337-8	Sequence 8, Appli
17	299.5	39.7	448	14	US-10-032-585-7660	Sequence 7660, Ap
18	281	37.2	497	14	US-10-128-714-8211	Sequence 8211, Ap
19	266.5	35.3	519	15	US-10-369-493-3786	Sequence 3786, Ap
20	265.5	35.2	589	15	US-10-395-027-1371	Sequence 1371, Ap
21	265	35.1	215	12	US-10-395-463-38	Sequence 38, Appl
22	262.5	34.8	415	14	US-10-128-714-3211	Sequence 3211, Ap
23	252.5	33.4	438	8	US-08-879-337-4	Sequence 4, Appli
24	252.5	33.4	438	15	US-10-369-493-1944	Sequence 1944, Ap
25	250	33.1	450	15	US-10-224-880C-22	Sequence 22, Appl
26	250	33.1	471	12	US-10-425-114-59752	Sequence 59752, A
27	250	33.1	476	12	US-10-425-114-42571	Sequence 42571, A
28	248	32.8	430	12	US-10-425-114-63907	Sequence 63907, A
29	247	32.7	430	15	US-10-224-880C-18	Sequence 18, Appl
30	243.5	32.3	432	12	US-10-424-599-192234	Sequence 192234,
31	243.5	32.3	432	15	US-10-224-880C-20	Sequence 20, Appl
32	237	31.4	473	15	US-10-369-493-21950	Sequence 21950, A
33	233	30.9	473	8	US-08-879-337-7	Sequence 7, Appli
34	225	29.8	432	9	US-09-817-774-29	Sequence 29, Appl
35	225	29.8	432	9	US-09-817-774-39	Sequence 39, Appl
36	225	29.8	432	9	US-09-817-774-45	Sequence 45, Appl
37	211	27.9	430	15	US-10-224-880C-31	Sequence 31, Appl
38	209.5	27.7	501	15	US-10-369-493-13025	Sequence 13025, A
39	205	27.2	453	8	US-08-879-337-6	Sequence 6, Appli
40	205	27.2	453	15	US-10-369-493-2273	Sequence 2273, Ap
41	197	26.1	476	9	US-09-817-774-31	Sequence 31, Appl
42	183	24.2	470	15	US-10-369-493-3263	Sequence 3263, Ap
43	172	22.8	307	12	US-10-395-463-32	Sequence 32, Appl
44	168	22.3	411	9	US-09-817-774-43	Sequence 43, Appl
45	164	21.7	408	9	US-09-817-774-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-10-425-114-66797
; Sequence 66797, Application US/10425114
; Publication NO. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425-114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73428
; SEQ ID NO 66797
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4746-067-F5_FLI.pep
US-10-425-114-66797

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QY	5	KNKVELSLGLANLCIFLIGYLVGRGANKQKHVKPKAPIWGKPKVVGKLLASGY	64				
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: S14R-YEAST
US-09-817-774-25

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QY      64 YWGTAHCNVLGDLALLSFLPCGVSSVVPYPTVLLILLVLRERRDEARCSQKYRI 123
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Db      408 WEKYCKAVKRIIPYVY 424

RESULT 10
US-10-369-493-22601
; Sequence 22601, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22601
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-10-369-493-22601

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Best Local Similarity 48.9%; Pred. No. 1e-30;
Matches 67; Conservative 22; Mismatches 43; Indels 5; Gaps 2;

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Db      408 WEKYCKAVKRIIPYVY 424

RESULT 11
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; Sequence 23, Application US/09817774
; Patent No. US2002012011A1
; GENERAL INFORMATION:
; APPLICANT: CHOE, Sunghwa
; APPLICANT: FELDMANN A., Kenneth
; TITLE OF INVENTION: DWIS MUTANTS
; FILE REFERENCE: 2225-0020 / 91020.002
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; CURRENT APPLICATION NUMBER: US/09/817,774
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/192,202
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 23
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LBR-RAT
US-09-817-774-23

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QY      19 LCIFLIGYLVFRGANKQKHVFKK--DPKAPITWGGPKPVVGGKLLASGYWGIARHCNYLG 75
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QY      76 DLLLALSFLPCGVSSVVPYPTVLLILLVLRERRDEARCSQKYRIWAEYCKLVPRRI 135
Db      363 DLIMALAWSLPCGFNHILPYFYVYFTALLTHREARDEHQCRRKYGLAWEKYQORVYRI 422

QY      136 LPYVY 140
Db      423 FPIYI 427

RESULT 12
US-09-729-674-142
; Sequence 142, Application US/09729674
; Patent No. US20010039335A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steinger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 6055-64X
; CURRENT APPLICATION NUMBER: US/09/729,674
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 09/539,330
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 283
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 142
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-729-674-142

Query Match      42.3%; Score 319.5; DB 9; Length 475;
Best Local Similarity 43.2%; Pred. No. 4.2e-28;
Matches 63; Conservative 26; Mismatches 44; Indels 13; Gaps 2;

QY      8 VELSLGLANLCIFLIGYLVFRGANKQKHVFKK-DPKAPITWGGPKPVV-----55
Db      330 VQLSTPHAVGVLLGLGVYIFRVANHQKDLFRDTGRCILWGRKPKVICSYTSADGQR 389
QY      56 -GGKLLASGYWGIARHCNCGDLLLALSLPCGVSSVVPYPTVLLILLVLRERDEA 114
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2004, 10:02:37 ; Search time 339.411 Seconds
(without alignments)
1882.767 Million cell updates/sec

Title: US-10-069-427-6
Perfected score: 755
Sequence: 1 PRVRKNKVELSLGLANLC.....REIWASYCKLVPRILPYVY 140

Scoring table: BLOSUM62

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Fgapop 6.0 , Fgapext 7.0
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Searched: 2998549 seqs, 2282253817 residues

Total number of hits satisfying chosen parameters: 5997098

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published Applications NA:

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- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq*
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- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
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3	496	65.7	2975	8	US-08-879-337-10	Sequence 10, Appl
4	496	65.7	6587	8	US-08-879-337-3	Sequence 3, Appli
5	431	57.1	707	13	US-10-424-599-133118	Sequence 133118, A
6	384.5	50.9	1473	13	US-10-425-114-30215	Sequence 30215, A
7	366	48.5	1443	17	US-10-648-593-128	Sequence 128, App
8	341.5	45.2	1272	16	US-10-369-493-46288	Sequence 46288, A
9	338	44.8	2100	16	US-10-295-027-1154	Sequence 1154, App
10	319.5	42.3	2481	9	US-09-729-674-141	Sequence 141, App
11	319.5	42.3	2597	13	US-10-342-887-599	Sequence 599, App
12	319.5	42.3	2597	13	US-10-172-118-599	Sequence 599, App
13	319.5	42.3	2597	17	US-10-429-160-31	Sequence 31, Appl
14	312.5	41.4	607	13	US-10-027-632-134379	Sequence 134379, A
15	312.5	41.4	607	13	US-10-027-632-134380	Sequence 134380, A
16	312.5	41.4	607	16	US-10-027-632-134379	Sequence 134379, A
17	312.5	41.4	607	16	US-10-027-632-134380	Sequence 134380, A
18	305.5	40.5	1546	16	US-10-264-049-46	Sequence 46, Appl
19	302	40.0	458	9	US-09-880-107-1079	Sequence 1079, App
20	299.5	39.7	1347	15	US-10-032-585-6660	Sequence 6660, Ap
21	293.5	38.9	428	9	US-09-922-217-71	Sequence 71, Appl
22	293.5	38.9	428	9	US-09-833-263-71	Sequence 71, Appl
23	293.5	38.9	428	14	US-10-025-380-71	Sequence 71, Appl
24	281	37.2	1494	15	US-10-128-714-7211	Sequence 7211, Ap
25	281	37.2	1614	15	US-10-128-714-6211	Sequence 6211, Ap
26	281	37.2	3814	15	US-10-128-714-5211	Sequence 5211, Ap
27	269.5	35.7	3242	15	US-10-128-714-211	Sequence 211, App
28	266.5	35.3	1557	16	US-10-369-493-27473	Sequence 27473, A
29	265.5	35.2	548	13	US-10-240-425-732	Sequence 732, App
30	265	35.1	645	13	US-10-395-463-37	Sequence 37, Appl
31	262.5	34.8	1245	15	US-10-128-714-2211	Sequence 2211, Ap
32	252.5	33.4	1317	16	US-10-369-493-25631	Sequence 25631, A
33	250	33.1	1895	16	US-10-224-880C-21	Sequence 21, Appl
34	250	33.1	1733	13	US-10-425-114-4603	Sequence 4603, Ap
35	250	33.1	1744	13	US-10-425-114-25988	Sequence 25988, A
36	248	32.8	1704	13	US-10-425-114-27671	Sequence 27671, A
37	247	32.3	1870	16	US-10-224-880C-17	Sequence 17, Appl
38	243.5	32.3	1646	16	US-10-224-880C-19	Sequence 19, Appl
39	243.5	32.3	1721	13	US-10-424-599-49392	Sequence 49392, A
40	237	31.4	1422	16	US-10-369-493-45637	Sequence 45637, A
41	234	31.0	221	8	US-08-879-337-23	Sequence 23, Appl
42	231	30.6	376	9	US-09-770-791-254	Sequence 254, App
43	225	29.8	588	13	US-09-770-152-90	Sequence 90, Appl
44	225	29.8	1299	9	US-09-938-842A-2112	Sequence 2112, Ap
45	225	29.8	1299	11	US-09-938-842A-2112	Sequence 2112, Ap

ALIGNMENTS

RESULT 1

US-10-425-114-28189

Sequence 28189, Application US/10425114

Publication No. US2004003488A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 28189

LENGTH: 1566

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: LIB4746-067-F5_FLI

US-10-425-114-28189

Alignment Scores:

Pred. No.: 1.7e-91 Length: 1566
 Score: 728.00 Matches: 134
 Percent Similarity: 100.00% Conservatives: 2
 Best Local Similarity: 98.53% Mismatches: 0
 Query Match: 96.42% Indels: 0
 DB: 13 Gaps: 0

US-10-069-427-6 (1-140) x US-10-425-114-28189 (1-1566)

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 QY 25 GlyTyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspProLys 44
 DB 1092 GGCTACCTAGTGTCCGAGGAGCTAACAGCAAAACATATGTTCAAGAGGACCCCAAA 1151
 QY 45 AlaProIleTTPGlyLysProProLysValValGlyClyLysLeuLeuAlaSerGlyTyr 64
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 QY 85 LeuProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuLeuLeu 104
 DB 1272 TTGCCCTGTGAGTGAGTTCGGTGCTCCCACTTCTACCCACGACTGCTCAATTCTA 1331
 QY 105 LeuValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluLeuTTP 124
 DB 1332 CTGCTCTTGAGGAAGCGCGATGAGCGGAGTGCTCGCAGAGTACAGGGAGATCTGG 1391
 QY 125 AlaGluTyrCysLysLeuValProTTPArgIleLeuProTyrValTyr 140
 DB 1392 GCAGGTACTGCAAGCTCGTGGCGTGAGGATCTGCTTATTGTTGAT 1439

RESULT 2

US-08-879-337-1
 ; Sequence 1, Application US/08879337A
 ; Publication No. US20030126630A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jang, Jyan-Chyun
 ; APPLICANT: Sheen, Jen
 ; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
 ; FILE REFERENCE: 00786/338001
 ; CURRENT APPLICATION NUMBER: US/08/879,337A
 ; CURRENT FILING DATE: 1997-06-20
 ; EARLIER APPLICATION NUMBER: 60/022,086
 ; EARLIER FILING DATE: 1996-06-21
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 1429
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (84)...(1189)
 ; NAME/KEY: variation
 ; LOCATION: (1)...(1429)
 ; OTHER INFORMATION: N can be any nucleotide.

Alignment Scores:

Pred. No.: 7.55e-75 Length: 1429
 Score: 609.00 Matches: 107
 Percent Similarity: 90.37% Conservatives: 15
 Best Local Similarity: 79.26% Mismatches: 13
 Query Match: 80.66% Indels: 0

DB: 8 Gaps: 0

US-10-069-427-6 (1-140) x US-08-879-337-1 (1-1429)

QY 6 AsnLysValGluLeuSerLeuSerGlyLeuAlaAsnLeuCysIlePheLeuLeuGly 25
 DB 786 AACAAAGTAGAAGTAAACAGTTCCTCGGATTGTAGTCAATTGCCTTGTCTTTGATAGGG 845
 QY 26 TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspProLysAla 45
 DB 846 TACATGGTTTTTCGAGGAGCTAACAAACAAACATATCTTTAAGAGAACCCCAAAACA 905
 QY 46 ProIleTTPGlyLysProProLysValValGlyClyLysLeuLeuAlaSerGlyTyrTTP 65
 DB 906 CCAATATGGGCAAGCCCTCCAGTGTAGTTGGTGAAGATTACTGGTTTCAGGCTATTGG 965
 QY 66 GlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeu 85
 DB 966 GGAATTGCAAGCACTGTAATTACTTGGCGACTTGATGCTTGTCTTCTCAGTTTG 1025
 QY 86 ProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuLeuLeu 105
 DB 1026 CCATGTGGAATAAGTTCTCCGGTTCCATATTCTACCCGATATACCTTCTGATATATTG 1085
 QY 106 ValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluLeuTTPAla 125
 DB 1086 ATATGGAGAGAACGAGAGACGAGTTCGATGTCAGAGAGTACAGGAGATATGGCA 1145
 QY 126 GluTyrCysLysLeuValProTTPArgIleLeuProTyrValTyr 140
 DB 1146 GAGTATCTTAGACTGTCCCTCGGAGAACTATCTCTTATGTTTAT 1190

RESULT 3

US-08-879-337-10
 ; Sequence 10, Application US/08879337A
 ; Publication No. US20030126630A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jang, Jyan-Chyun
 ; APPLICANT: Sheen, Jen
 ; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
 ; FILE REFERENCE: 00786/338001
 ; CURRENT APPLICATION NUMBER: US/08/879,337A
 ; CURRENT FILING DATE: 1997-06-20
 ; EARLIER APPLICATION NUMBER: 60/022,086
 ; EARLIER FILING DATE: 1996-06-21
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 2975
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: variation
 ; LOCATION: (1)...(2975)
 ; OTHER INFORMATION: N can be any nucleotide.

Alignment Scores:

Pred. No.: 1.61e-58 Length: 2975
 Score: 496.00 Matches: 107
 Percent Similarity: 44.49% Conservatives: 14
 Best Local Similarity: 39.34% Mismatches: 14
 Query Match: 65.70% Indels: 137
 DB: 8 Gaps: 3

US-10-069-427-6 (1-140) x US-08-879-337-10 (1-2975)

QY 6 AsnLysValGluLeuSerLeuSerGlyLeuAlaAsnLeuCysIlePheLeuLeuGly 25
 DB 2007 AACAAAGTAGAAGTAAACAGTTCCTCGGATTGTAGTCAATTGCCTTGTCTTTGATAGGG 2066
 QY 25 Y----- 25

Db 2067 TAAGTCTGAGACATGGGGTATTTCCATTTCTACATATCTACACTAAGAAACCCACTA 2126
Qy 26 -----TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPhe 40
Db 2127 TTTCTCTTTGGCAGGTACATGGTTTTCGAGGAGCTAACAAACAAACATATCTTTAA 2186
Qy 40 sLysAspProLysAlaProIleTrpGlyLysProLysValValGlyGlyLysLeu 60
Db 2187 GAGAACCCAAACACCAATATGGGCAAGCCTCCAGTGTAGTTGGTGAAGTACT 2246
Qy 60 uAlaSerGlyTyrTrp ----- 65
Db 2247 GGTTCAGGCTATTGGTATGTTATTTATCTCTCTGTTCTTTCTGTTGTTTCGCCA 2306
Qy 65 ----- 65
Db 2307 TCTCTGTGTTGATTGTTTCATCATGCTGGGAATAAGAGTTGAAAGTTCGCCAATGACAC 2366
Qy 66 -----GlyIleAlaArgHisCysAs 72
Db 2367 ATTTCGGATAACTTAGTGTGTTTGTATATATGACAGGGGAATTGCAAGGCACTGTAA 2426
Qy 72 nTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeuProCysGlyVal ----- 89
Db 2427 TTACCTTGGGCACTGTATGCTGTCTCTTCACTTTCGCAATGTTGAATAAGTACTC 2486
Qy 89 ----- 89
Db 2487 CTNCTGCTGATGATTCACCTACAGCTACCAAAATCATGTAGAAACTAATACCAATATCNA 2546
Qy 89 ----- 89
Db 2547 ACGTTCGAAGTTGATTGGCTGACTTAAAGATATGTATCTTAACCATCATTTGAAAGT 2606
Qy 89 ----- 89
Db 2607 CTAAGCTTCAAGTTCATTTCCAAAGCTGTTTTHATGATATTTGCTCTNGTGTATCT 2666
Qy 90 -SerSerValValProTyrPheTyrProThrTyrLeuLeuLeuValLeuArgG 109
Db 2667 CAGTTCTCCGTTCCATATTTCTACCCGATATACCTGCTGATATTTGATATGGAGAGA 2726
Qy 109 uArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTrpAlaGluTyrCysLy 129
Db 2727 ACGAAGAGCAAGTTCGATGTGCAGAGAAGTACNAGGAGATATGGGCAGATATCTTAG 2786
Qy 129 sLeuValProTyrPheArgGlyLeuProTyrValTyr 140
Db 2787 ACTTGTCCTCGGAGATACTTCTCTTATGTTAT 2820

RESULT 4

US-08-879-337-3
; Sequence 3, Application US/08879337A
; Publication No. US20030126630A1
; GENERAL INFORMATION:
; APPLICANT: Jang, Jyan-Chyun
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USBS THEREOF
; FILE REFERENCE: 00786/338001
; CURRENT APPLICATION NUMBER: US/08/879,337A
; CURRENT FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/022,085
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 6587
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)...(6587)
; OTHER INFORMATION: N can be any nucleotide.

US-08-879-337-3
Alignment Scores:
Pred. No.: 5,17e-58 Length: 6587
Score: 496.00 Matches: 107
Percent Similarity: 44.49% Conservative: 14
Best Local Similarity: 39.34% Mismatches: 14
Query Match: 65.70% Indels: 137
DB: 8 Gaps: 3

US-10-069-427-6 (1-140) x US-08-879-337-3 (1-6587)

Qy 6 AsnLysValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuLeu-Gl 25
Db 5361 AACAAAGTAGAAGTAACTAACAAATTCCTCGGATTTGAGTCAATTCCTTGTCTCTTGTAGGG 5420
Qy 25 Y----- 25
Db 5421 TAAGTTCTGAGACATGGGGTTATTTTCATCTTTTACATATCTACACTAAGAAACCCACTA 5480
Qy 26 -----TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPhe 40
Db 5481 TTTCTCTTTGGCAGGTACATGGTTTTCGAGGAGCTAACAAACAAACATATCTTTAA 5540
Qy 40 sLysAspProLysAlaProIleTrpGlyLysProLysValValGlyGlyLysLeu 60
Db 5541 GAAGAACCCAAACACCAATATGGGCAAGCCTCCAGTGTAGTTGGTGAAGTACT 5600
Qy 60 uAlaSerGlyTyrTrp ----- 65
Db 5601 GGTTCAGGCTATTGGTATGTTATTTATCTCTCTGTTGTTTCTGTTGTTTCGCCA 5660
Qy 65 ----- 65
Db 5661 TCTCTGTGTTGATTGTTTCATCATGCTGGGAATAAGAGTTGAAAGTTCGCCAATGACAC 5720
Qy 66 -----GlyIleAlaArgHisCysAs 72
Db 5721 ATTTCGGATAACTTAGTGTGTTTGTATATATGACAGGGGAATTGCAAGGCACTGTAA 5780
Qy 72 nTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeuProCysGlyVal ----- 89
Db 5781 TTACCTTGGGCACTGTATGCTGTCTCTTCACTTTCGCAATGTTGAATAAGTACTC 5840
Qy 89 ----- 89
Db 5841 CTNCTGCTGATGATTCACCTACAGCTACCAAAATCATGTAGAAACTAATACCAATATCNA 5900
Qy 89 ----- 89
Db 5901 ACGTTCGAAGTTGATTGGCTGACTTAAAGATATTTGATCTCTAACCATCATTTGAAAGT 5960
Qy 89 ----- 89
Db 5961 CTAAGCTTTCAGTTCATTTCCCAAGCTGTTTTTATGATATTTGCTCTNGTGTATCT 6020
Qy 90 -SerSerValValProTyrPheTyrProThrTyrLeuLeuLeuValLeuArgG 109
Db 6021 CAGTTCTCCGTTCCATATTTCTACCCGATATACCTGCTGATATTTGATATGGAGAGA 6080
Qy 109 uArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTrpAlaGluTyrCysLy 129
Db 6081 ACGAAGAGCAAGTTCGATGTGCAGAGAAGTACNAGGAGATATGGGCAGATATCTTAG 6140
Qy 129 sLeuValProTyrPheArgGlyLeuProTyrValTyr 140
Db 6141 ACTTGTCCTCGGAGATACTTCTCTTATGTTAT 6174

RESULT 5

US-10-424-599-133118/c
; Sequence 133118, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 133118
 ; LENGTH: 707
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_91211C.1
 US-10-424-599-133118

Alignment Scores:
 Pred. No.: 2,62e-50 Length: 707
 Score: 431.00 Matches: 76
 Percent Similarity: 94.32% Conservative: 7
 Best Local Similarity: 86.36% Mismatches: 5
 Query Match: 57.09% Indels: 0
 DB: 13 Gaps: 0

US-10-069-427-6 (1-140) x US-10-424-599-133118 (1-707)

QY 53 LysValValGlyGlyLysLeuLeuAlaSerGlyTyrTrpGlyLeuAlaArgHisCysAsn 72
 Db 700 AAGTCATGTTGGTGAAGCTACTCTTCTTCTGTTATTTGGGTATTTCTAGACACTGTAT 641
 QY 73 TyrLeuGlyAspLeuLeuLeuAlaLeuSerPheSerLeuProCysGlyValSerVal 92
 Db 640 TACCTAGGGATTGATGCTGCTCTCTCTTACCTTACCATGTTGGGATAAGTTCCACCA 581
 QY 93 ValProTyrPheTyrProTyrTyrLeuLeuLeuValLeuArgGluArgAsp 112
 Db 580 ATTCATCTACTTATCAATTTATCTTCTTATCTGTTATCTGGAGAGAGAGAGGAT 521
 QY 113 GluAlaArgCysSerGlnLysTyrArgGluLeuTyrAlaGluTyrCysLysLeuValPro 132
 Db 520 GAACCTGTTGGCGGAGAGATAGAGAGATATGGCCGAGTATCGTAACTTGTTCACCA 461
 QY 133 TrpArgLeuProTyrValTyr 140
 Db 460 TGGAGAATATGCTTACGTTTAT 437

RESULT 6
 US-10-425-114-30215
 ; Sequence 30215, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 30215
 ; LENGTH: 1473
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: UC-OSROM202008A09_FLI
 US-10-425-114-30215

Alignment Scores:
 Pred. No.: 2,59e-43 Length: 1473
 Score: 384.50 Matches: 77
 Percent Similarity: 65.00% Conservative: 14
 Best Local Similarity: 55.00% Mismatches: 36
 Query Match: 50.93% Indels: 13
 DB: 13 Gaps: 2

US-10-069-427-6 (1-140) x US-10-425-114-30215 (1-1473)

QY 9 GluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysLeuPheLeuLeuGlyTyrLeuVal 28
 Db 999 GAGCTGTGAGGCTGGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 1058
 QY 29 PheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspProLysAlaProIleTyr 48
 Db 1059 TTCGGGGGGCAACGGGCAAGAGCGCTTCAGCGGGGACCG----- 1103
 QY 49 GlyLysPro-----ProlysValValGlyGlyLysLeuLeu 60
 Db 1104 GGCCACCCCTCTGTGGCGCACTGTGCAGAGCATGCCCACTGTGGCGGGCACGCGCTGCTG 1163
 QY 61 AlaSerGlyTyrTrpGlyLeuAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAla 80
 Db 1164 ATTACGGCTACTGTGGGCTATGGCCGCACATCACTACCTGGGGGACTGGCTCATGGC 1223
 QY 81 LeuSerPheSerLeuProCysGlyValSerValValProTyrPheTyrProTyrTyr 100
 Db 1224 CTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1283
 QY 101 LeuLeuLeuLeuValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyr 120
 Db 1284 TTTGCCAGCTGCTGTGTGCACAGGGAGCGGGGATGAGCGGCTCCCGCTGAAGTAC 1343
 QY 121 ArgGluLeuTyrAlaGluTyrCysLysLeuValProTyrPheTyrValTyr 140
 Db 1344 GGGCGGAGCTGGCAAGTACTGTGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1403

RESULT 7
 US-10-648-593-128
 ; Sequence 128, Application US/10648593
 ; Publication No. US20040106132A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
 ; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
 ; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
 ; FILE REFERENCE: D0273 NP
 ; CURRENT APPLICATION NUMBER: US/10/648,593
 ; CURRENT FILING DATE: 2003-08-26
 ; PRIOR APPLICATION NUMBER: 60/406,385
 ; PRIOR FILING DATE: 2002-08-27
 ; NUMBER OF SEQ ID NOS: 557
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 128
 ; LENGTH: 1443
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-648-593-128

Alignment Scores:
 Pred. No.: 9,93e-41 Length: 1443
 Score: 366.00 Matches: 69
 Percent Similarity: 70.63% Conservative: 20
 Best Local Similarity: 54.76% Mismatches: 33
 Query Match: 48.48% Indels: 4
 DB: 17 Gaps: 3

US-10-069-427-6 (1-140) x US-10-648-593-128 (1-1443)
 QY 19 LeuCysIlePhe---LeuIleGlyTyrLeuValPheArgGlyAlaAsnLysGlnLysHis 37
 Db 1003 ATCTGCTCATCATGCTATTGTTACTACATCTCTCTGTTGGGCGGATTCACGAAAC 1062

Qy	19	LeuCysIlePhe---LeuIleGlyTyrLeuValPheArgGlyAlaAsnLysGlnLysHis	37
Db	1533	ATTCGCTCATCAATGCTACTGTTACTACATCTTCGCTGGGGCGAATCCCGAGAAAAC	1592
Qy	38	ValPheIlysIysAspProLysAlaPro---IleTrpGlyLysPro-----ProLysVal	54
Db	1593	ACITTCGGAAGAATCCCTCTGACCCAGAGTGGCTGGGCTTGAGACCATCTCTACAGCC	1652
Qy	55	ValGlyGlyLysLeuLeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeu	74
Db	1653	ACAGGGCGGAACTGCTGGTGTCTGGGTGGTGGGTATGTCGCCCATCCCACTATCTT	1712
Qy	75	GlyAspLeuLeuAlaLeuSerPheSerLeuProCysGlyValSerSerValValPro	94
Db	1713	GGAGACCTCATATGGCTCTGGCTGTGCTCCCTCGGGGTGTCAACACTGCTGCC	1772
Qy	95	TyrPheTyrProThrTyrLeuLeuIleLeuLeuValLeuArgGluArgAspGluAla	114
Db	1773	TACTTCTACTCTCTCTACTTACCGCGCTGCTGGTGACCGTGAGGCCCGGAGTAGCG-	1831
Qy	115	ArgCysSerGlnLysTyrArgGluIleTrpAlaGluTyrCysLysLeuValProTyrArg	134
Db	1832	GAGTGGCTCAGAAAGTACGGCCTGGCCTGCGAGGAGTACTCCGGCGGTGTCCTTACCG	1891
Qy	135	IleLeuProTyrValTyr	140
Db	1892	ATCATGCCCTACATCTAC	1909

```

RESULT 10
US-09-729-674-141
; Sequence 141, Application US/09729674
; Patent No. US2001003935A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Pechtel, Kim
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 6055-64X
; CURRENT APPLICATION NUMBER: US/09/729,674
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 09/539,330
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 283
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 141
; LENGTH: 2481
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-729-674-141

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1065	Db	GTGCACTGTCCACCCCGCAGCGCGGTGGGGTCTCTGCTGGCGCTGTGGCGCTACTAC	1124
28	Qy	ValPheArgGlyAlaAsnLysGlnLysHisValPheLysLys---AspProLysAlaPro	46
1125	Db	ATCTTCGGGTGGCCAAACACCAAGAGGACCTGTTCCGCGCGCAGGATGGCGCTGCCTC	1184
47	Qy	IleTrpGlyLysProProLysValVal-----	55
1185	Db	ATCTGGGGCAGGAAGCCCAAGGTCTATCGAGTGTCTACACATCCGCCGACGGGCAGAGG	1244
56	Qy	---GlyGlyLysLeuLeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeu	74
1245	Db	CACCACGACGAGCTGCTGGTGTGGCGCTTCGGGGCGTGGCCGCCACCTTCACTACGCTC	1304
75	Qy	GlyAspLeuLeuAlaLeuSerPheSerLeuProCysGlyValSerValValPro	94
1305	Db	GGCGACCTGATGGGCAGCCTGGCCTACTGCTGGCGTGTGGCGGTGGCCACCTGTGCC	1364
95	Qy	TyrPheTyrProThrTyrLeuLeuIleLeuLeuValLeuArgGluArgAspGluAla	114
1365	Db	TACTTCTACATCATCATGACATGCCATCCTCTGCTGACCCACCGTGTCTCCGGGACGAGCAC	1424
115	Qy	ArgCysSerGlnLysTyrArgGluIleTrpAlaGluTyrCysLysLeuValProTrpArg	134
1425	Db	CGTGGCCGACGAGTACCGCGCGGACTGGAGCGCTACACCGCCGACGTGCCTTACCGC	1484
135	Qy	IleLeuProTyrValTyr	140
1485	Db	CTGCTCCCTGGATCTTC	1502

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RESULT 11
US-10-342-887-599
; Sequence 599, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Kinsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernard, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/390,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 599
; LENGTH: 2597
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-599

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Db 1362 CACCACAGCAGTCTGCTGGGCTTCTGGGGCGTGGCCCGCCACTTCACTAGCTC 1421
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 75 GlyAspLeuLeuAlaLeuSerPheSerLeuProCysGlyValSerValPro 94
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1422 GCGCAGCTGATGGGCGACCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1481
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 95 TyrPheTyrProThrTyrLeuLeuLeuValLeuArgGluArgAspGluAla 114
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1482 TACTTTCATCATCTACATGCGCATCTGCTGACCCACCGCTGCTCCGGAGCAGCAC 1541
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 115 ArgCysSerGlnLysTyrA-gluiletrpAlaGluTyrCysLysLeuValProTrpArg 134
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1542 CGCTGGCCAGCAAGTACGGCGGAGCTGGAGCGCTACACCGCGCAGTGCCTTACCGC 1601
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 135 IleLeuProTyrValTyr 140
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1602 CTGCTGGCTGGAATCTTC 1619
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-10-027-632-134379
; Sequence 134379, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134379
; LENGTH: 607
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-134379

Alignment Scores:
Pred. No.: 9,04e-34 Length: 607
Score: 312.50 Matches: 60
Percent Similarity: 62.22% Conservativeness: 24
Best Local Similarity: 44.44% Mismatches: 38
Query Match: 41.39% Indels: 13
DB: 2 Gaps: 2

US-10-069-427-6 (1-140) x US-10-027-632-134379 (1-607)
Qy 19 LeuCysIlePheLeuIleGlyTyrLeuValPheArgGlyAlaAsnLysGlnLysHisVal 38
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RESULT 15
US-10-027-632-134380
; Sequence 134380, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134380
; LENGTH: 607
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-134380

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Score: 312.50 Matches: 60
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Query Match: 41.39% Indels: 13
DB: 2 Gaps: 2

US-10-069-427-6 (1-140) x US-10-027-632-134380 (1-607)
Qy 19 LeuCysIlePheLeuIleGlyTyrLeuValPheArgGlyAlaAsnLysGlnLysHisVal 38
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Db 24 CTGCTGCTGGCGCTGGTGGCTACTACATCTTCCGGGTGGCCACCAAGAGGACCTG 83
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Qy 66 GlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeu 85
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Qy	106	ValLeuArgGluArgArgAspGluAlaArgCysSerGlnLysTyrArgGluLeu	125
Db	324	ACCCACCGCTGCCCTCCGGGACGAGACCGCTGGCCAGCAAGTACGGCCGGGACT	383
Qy	126	GluTyrCysLysLeuValProTyrArgIleLeuProTyrValTyr	140
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Search completed: June 14, 2004, 16:03:04
Job time : 343.411 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2004, 09:48:07 ; Search time 2238.35 Seconds

(without alignments)
2710.937 Million cell updates/sec

Title: US-10-069-427-6

Perfect score: 755

Sequence: 1 PRVRKNKVELLSGLANLC.....REIMAEYCKLVPRILPYVY 140

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
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36: em_htg_mam.*
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39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	755	100.0	667	6	AX107837 Sequence
2	638	84.5	604	6	ARI74091 Sequence
3	627	83.0	1631	6	AX107835 Sequence
4	621	82.3	1364	6	AX107839 Sequence
5	609	80.7	1110	8	AY133650 Arabidops
6	609	80.7	1413	8	AF256535 Arabidops
7	609	80.7	1429	6	AR427911 Sequence
8	609	80.7	1429	8	AF257178 Arabidops
9	609	80.7	1449	8	AY064964 Arabidops
10	595.5	78.9	1456	8	AX112105 Oryza sat
11	497.5	65.9	2828	8	AF263244 Arabidops
12	497.5	65.9	3992	8	AF256536 Arabidops
13	496	65.7	99814	8	AF263244 Arabidops
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15	471.5	62.5	141428	6	AP005558 Oryza sat
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17	471.5	60.0	120593	8	AP002870 Oryza sat
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19	453	58.5	572	6	ARI74092 Sequence
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23	374.5	49.6	2657	5	BC055976 Xenopus l
24	366	48.5	1443	9	AF096304 Homo sapi
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26	365	48.3	1203	3	AF308470 Dictyoste
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28	357.5	47.4	3759	9	BC020079 Homo sapi
29	356.5	47.2	3714	6	AX375034 Sequence
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31	355	47.0	413	6	ARI74090 Sequence
32	354	46.9	1370	4	AY039681 Bos tauru
33	343	45.4	1523	10	BC014769 Mus muscu
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35	341.5	45.2	37852	8	SPBC16G5 S.pombe c
36	338.5	44.8	1108	10	BC014835 Mus muscu
37	338	44.8	2100	6	AX658185 Sequence
38	338	44.8	2100	9	AF023676 Homo sapi
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40	332.5	44.0	2160	5	XLA17842 Xenopus lae
41	332.5	44.0	2319	10	BC042522 Mus muscu
42	332.5	44.0	2503	10	BC029171 Mus muscu
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ALIGNMENTS

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 VERSION AX107837.1 GI:13923233
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 ORGANISM
 Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE
 AUTHORS Famodu, O.O. and Kinney, A.J.
 TITLE Genes encoding sterol delta-15 reductase in plants
 JOURNAL Patent: WO 0123539-A 5 05-APR-2001;
 E.I. DU PONT DE NEMOURS AND COMPANY (US)
 FEATURES
 source Location/Qualifiers
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 Db 301 CTGCTCATCTTACTGTTCTGAGGAAAGCGCGATGAGCGAGTGCTCGCAGAGATC 360
 QY 121 ArgGluIleTyrPheAlaGluTyrCysLysLeuValProTyrPheTyrValTyr 140
 Db 361 AGGAGATCTGGGACAGTACTGCAAGCTGCTGCGCGTGGAGGATCTGCTTATGTGTC 420
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 DEFINITION Sequence 3 from patent US 6306632.
 ACCESSION AR174091
 VERSION AR174091.1 GI:11791411
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown.
 Unclassified.
 REFERENCE
 1 (bases 1 to 604)
 AUTHORS Cahoon, R.E. and Rafalski, J. Antoni.

TITLE Chromatin associated proteins
 JOURNAL Patent: US 6306632-A 3 23-OCT-2001;
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 QY 45 AlaProIleTyrGlyLysProLysValValGlyLysLeuAlaSerGlyTyr 64
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 LOCUS AX107835 1631 bp DNA linear PAT 30-APR-2001
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 VERSION AX107835.1 GI:13923232
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 ORGANISM
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 Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 REFERENCE
 1
 AUTHORS Famodu, O.O. and Kinney, A.J.
 TITLE Genes encoding sterol delta-15 reductase in plants
 JOURNAL Patent: WO 0123539-A 3 05-APR-2001;
 E.I. DU PONT DE NEMOURS AND COMPANY (US)
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Karlin-Neumann, G., Lam, B., Lee, J. M., Lin, J., Miranda, M., Nguyen, M., Onodera, C. S., Palm, C. J., Quach, H. L., Southwick, A., Tang, C. C., Toriumi, M., Wu, H. C., Yamada, K., Yamamura, Y., Yu, G., Davis, R. W., Theologis, A., and Ecker, J. R.

Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J. R. (SSP/Salk) contributed equally to this work as PIs.

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source

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ORIGIN

Alignment Scores:
Pred. No.: 1,23e-60 Length: 1110
Score: 609.00 Matches: 107
Percent Similarity: 90.37% Conservatives: 15
Best Local Similarity: 79.26% Mismatches: 13
Query Match: 80.66% Indels: 0
DB: 8 Gaps: 0

US-10-069-427-6 (1-140) x AV133650 (1-1110)

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RESULT 6
AF256535 1413 bp mRNA linear PLN 09-JUL-2000
LOCUS

DEFINITION

Arabidopsis thaliana sterol C-14 reductase PACKEL (FK) mRNA, complete cds.

ACCESSION

AF256535

VERSION

AF256535.1 GI:8980703

KEYWORDS

Arabidopsis thaliana (thale cress)

SOURCE

Arabidopsis thaliana

ORGANISM

Arabidopsis thaliana
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REFERENCE

1 (bases 1 to 1413)

AUTHORS

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J., Schmidt, J., and Jurgens, G.

TITLE

PACKEL is a sterol C-14 reductase required for organized cell division and expansion in Arabidopsis embryogenesis

JOURNAL

Genes Dev. 14 (12), 1471-1484 (2000)

MEDLINE

20317031

PUBMED

10859166

REFERENCE

2 (bases 1 to 1413)

AUTHORS

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J., Schmidt, J., and Jurgens, G.

TITLE

Submitted (17-APR-2000) ZMBP, University of Tuebingen, Auf der Morgenstelle 1, Tuebingen D-72076, Germany

JOURNAL

Location/Qualifiers

FEATURES

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ORIGIN

Alignment Scores:
Pred. No.: 1,62e-60 Length: 1413
Score: 609.00 Matches: 107
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Best Local Similarity: 79.26% Mismatches: 13
Query Match: 80.66% Indels: 0
DB: 8 Gaps: 0

US-10-069-427-6 (1-140) x AF256535 (1-1413)

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Db 827 AACAAAGTAGAACCTAACAGTTCTCGGATTTGTAGTCAATTGCCTTCTTGTATAGG 886
Qy 26 TyrLeuValPheArgGlyValAsnLysGlnLysHisValPheLysLysAspProLysAla 45
Db 887 TACATGGTTTTCGAGGAGCTAACAAACAAACATATCTTTAAGAGAACCCAAACAA 946
Qy 46 ProfileTrpGlyLysProLysValValGlyLysLeuAlaSerGlyTyrTrp 65
Db 947 CCAATATGGGCAAGCCTCCAGTGGTGTAGTGGTGAAGTTACTGGTTTCAGGCTATTG 1006
Qy 66 GlvIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeu 85
Db 1007 GGAATTGCAAGCACTGTAATTTACTTGGGACTGTGCTTGTCTTCTTCACTTGG 1066

Qy 86 ProCysGlyValSerSerValProTyrPheTyrProThrTyrLeuLeuLeuLeuLeuLeu 105
Db 1067 CCATGTGGATAAGTTTCGGTTCCTATATTTTACCCTGATATACCTTCTGATACATTG 1126
Qy 106 ValLeuArgGluArgGAspGluAlaArgCysSerGlnLysTyrArgGluLeuLeuLeuLeu 125
Db 1127 ATATGGAGAGAACCAAGAGAGAGAGGTTTCGATGTCAGAGAGAGATACAGGAGATGGCA 1186
Qy 126 GluTyrCysLysLeuValProTyrPheTyrPheTyrPheTyrPheTyrPheTyrPheTyr 140
Db 1187 GAGTATCTTAGACTGTGCTCCCTGAGAAATACCTTCTTATGTTAT 1231
RESULT 7
AR427911
LOCUS AR427911 1429 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 2 from patent US 6639130.
ACCESSION AR427911
VERSION AR427911.1 GI:40186946
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1429)
AUTHORS Jang,J.-C. and Sheen,J.
TITLE Plant sterol reductases and uses thereof
JOURNAL Patent: US 6639130-A 2 28-OCT-2003;
FEATURES
Location/Qualifiers
source
/organism="unknown"
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ORIGIN
Alignment Scores:
Pred. No.: 1.64e-60 Length: 1429
Score: 609.00 Matches: 107
Percent Similarity: 90.37% Conservative: 15
Best Local Similarity: 79.26% Mismatches: 13
Query Match: 80.66% Indels: 0
DB: 6 Gaps: 0
US-10-069-427-6 (1-140) x AR427911 (1-1429)
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Db 786 AACAAAGTAGAACTAACAGTTCCTCGGATTGTAGTCAATTCCTTCTTCTGATAGGG 845
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Qy 106 ValLeuArgGluArgGAspGluAlaArgCysSerGlnLysTyrArgGluLeuLeuLeuLeu 125
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AF257178

LOCUS AF257178 1429 bp mRNA linear PLN 05-JUL-2000
DEFINITION Arabidopsis thaliana C-14 sterol reductase (PACKEL) mRNA, complete cds.
ACCESSION AF257178
VERSION AF257178.1 GI:8917584
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 1429)
AUTHORS Jang,J.C., Fujioka,S., Tasaka,M., Seto,H., Takatsuto,S., Ishii,A., Aida,M., Yoshida,S. and Sheen,J.
TITLE A critical role of sterols in embryonic patterning and meristem programming revealed by the fackel mutants of Arabidopsis thaliana
JOURNAL Genes Dev. 14 (12), 1485-1497 (2000)
MEDLINE 20317032
PUBMED 10859167
REFERENCE 2 (bases 1 to 1429)
AUTHORS Jang,J.-C. and Sheen,J.
TITLE Direct Submission
JOURNAL Submitted (17-APR-2000) Horticulture and Crop Science, The Ohio State University, 310A Kottman Hall, 2021 Coffey Road, Columbus, OH 43210, USA
FEATURES
Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 1.64e-60 Length: 1429
Score: 609.00 Matches: 107
Percent Similarity: 90.37% Conservative: 15
Best Local Similarity: 79.26% Mismatches: 13
Query Match: 80.66% Indels: 0
DB: 8 Gaps: 0
US-10-069-427-6 (1-140) x AF257178 (1-1429)
Qy 6 AsnLysValGluLeuSerLeuSerGlyLeuAlaAsnLeuCysIlePheLeuLeuGly 25
Db 786 AACAAAGTAGAACTAACAGTTCCTCGGATTGTAGTCAATTCCTTCTTCTGATAGGG 845
Qy 26 TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspProLysAla 45
Db 846 TACATGGTTTTCGAGAGGCTAACAAACAAACATATCTTTAGAAAGAACCCAAACAA 905
Qy 46 ProLeuTrpGlyLysProProLysValValGlyLysLeuLeuAlaSerGlyTyrTrp 65
Db 906 CCAATATGGGCAAGCCTCCAGTGTAGTTGGTGAAGTTACTGTTTCAGGCTATTGG 965
Qy 56 GlyTyrLeuAlaArgHisCysAsnTyrLeuGlyAspLeuLeuLeuLeuLeuLeuLeu 85
Db 966 GGAATTCGAGGCACTGAATTAATTCCTGGGCACTGATGCTGCTCTCTCAGTTG 1025

Qy 86 proCysGlyValserValProTyrPheTyrProThrTyrLeuLeuLeuLeu 105
 Db 1026 CCATGTGAATAGTCTCCGGTTCCATATTTACCGGATATACCTTCTGATACATTG 1085

Qy 106 ValLeuArgGluArgAAspGluAlaArgCysSerGlnLysTyrArgGluLeuLeuPala 125
 Db 1086 ATATGGAGAGAACGAGAGACGAGGTTGCGATGTCGAGAGAGTACCAAGGAGATATGGCA 1145

Qy 126 GluTyrCysLysLeuValProTyrArgIleLeuProTyrValTyr 140
 Db 1146 GAGTATCTTAGACTTGTCCCTCGGAGATATCTTCTTATGTTAT 1190

RESULT 9
 AY064964 1449 bp mRNA linear PLN 10-DEC-2001
 LOCUS Arabidopsis thaliana AT3G52940/F8J2_111 mRNA, complete cds.
 DEFINITION Arabidopsis thaliana (thale cress)
 ACCESSION AY064964
 VERSION AY064964.1 GI:17473515
 KEYWORDS FLI CDNA.
 ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 1449)
 AUTHORS Cheuk,R., Chen,H., Kim,C.J., Meyers,M.C., Banh,J., Bowser,L., Carninci,P., Chang,E., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.

TITLE Arabidopsis cDNA clones
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1449)
 AUTHORS Cheuk,R., Chen,H., Kim,C.J., Meyers,M.C., Banh,J., Bowser,L., Carninci,P., Chang,E., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.

TITLE Direct Submission
 JOURNAL Submitted (30-NOV-2001) Salk Institute Genomic Analysis Laboratory (SigNal), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

COMMENT RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGECC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Cheuk,R., Chen,H., Kim,C.J., Meyers,M.C., Shinn,P., Banh,J., Bowser,L., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Davis,R.W., Theologis,A., and Ecker,J.R.

Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk) contributed equally to this work as PIs.

LOCATION/Qualifiers
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 LMIPTFSIQGMULLHNKVELTIPVAVVNCVLVFLIGYVFRGAKQKHIFKQPKPI
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 1295. 1449

3'UTR
 ORIGIN

Alignment Scores:
 Pred. No.: 1.67e-60 Length: 1449
 Score: 609.00 Matches: 107
 Percent Similarity: 90.37% Conservative: 15
 Best Local Similarity: 79.26% Mismatches: 13
 Query Match: 80.66% Indels: 0
 DB: 8 Gaps: 0

US-10-069-427-6 (1-140) x AY064964 (1-1449)

Qy 6 AsnLysValGluLeuSerGlyLeuAlaAsnLeuLeuLeuLeuLeuLeu 25
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Qy 26 TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspProLysAla 45
 Db 947 TACATGGTTTTTCGAGGAGCTAACAAACAAACATATCTTTAAGAGAAGACCCAAAAACA 1006

Qy 46 ProIleTyrGlyLysProLysValValGlyLysLeuLeuAlaSerGlyTyrTyr 65
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Qy 66 GlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuLeuLeuLeuLeuSerPheSerLeu 85
 Db 1067 GCAATTGCAAGGCACTGTATTACCTTGGCGACTGTGCTGCTCTTCTTCTTCTTCTT 1126

Qy 86 ProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuLeuLeu 105
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Qy 106 ValLeuArgGluArgAAspGluAlaArgCysSerGlnLysTyrArgGluLeuLeuPala 125
 Db 1187 ATATGGAGAGAACGAGAGACGAGTTCGATGTCGAGAGAGTACCAAGGAGATATGGCA 1246

Qy 126 GluTyrCysLysLeuValProTyrArgIleLeuProTyrValTyr 140
 Db 1247 GAGTATCTTAGACTTGTCCCTCGGAGATATCTTCTTATGTTAT 1291

RESULT 10
 AK112105
 LOCUS Oryza sativa (japonica cultivar-group) cDNA clone:002-110-E10, full insert sequence.
 DEFINITION AK112105
 ACCESSION AK112105.1 GI:37988768
 KEYWORDS FLI CDNA; oligo capping.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1
 AUTHORS The Rice Full-length cDNA Consortium, National Institute of

JOURNAL	Genes Dev. 14 (12), 1485-1497 (2000)	QY	72	nTyrLeuGlyAspLeuLeuLeuAlaLeuSerPheSerLeuProCysGlyVal-----	89
MEDLINE	20317032	Db	2429	TTACCTTGGCAGCTGATGCTTGTCTGCTTGCATTTGCGAATAAGGTAAT	2488
PUBMED	10859167	QY	89	-----	89
REFERENCE	2 (bases 1 to 2828)	Db	2489	TCTTCTGCTTGAGTTCATCTTACAGCTACCAAAAGTCATGTAGAACTAATACCAATATC	2548
AUTHORS	Jang,J.C. and Sheen,J.	QY	89	-----	89
TITLE	Direct Submission	Db	2549	AAAACGTTTGAAGTTGATTGGCTGACTTAAAGATATTGATCTCTAACCATCATTTGAAA	2608
JOURNAL	Submitted (03-MAY-2000) Horticulture and Crop Science, The Ohio State University, 310A Kottman Hall, 2021 Coffey Rd, Columbus, OH 43210, USA	QY	89	-----	89
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	/mol_type="genomic DNA"	QY	108	gGluArgArgAspGluAlaArgCysSerGlnLysTyrArgGluLeuTrpAlaGluTyrCy	128
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		ORGANISM		Arabidopsis thaliana	
ORIGIN					
Alignment Scores:					
Pred. No.:	2,76e-47				
Score:	497.50				
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DB:	8				
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QY	25	Y-----			25
Db	2069	TAGTCTCGACATGGGTTATTTTCCATTCTTACATATCTACATAAGAACCCACTA			2128
QY	26	-----TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLys 40			
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QY	40	sLysAspProLysAlaProLysTrpGlyLysProProLysValValGlyLysLeuLe 60			
Db	2189	GAAGAACCAACCAACCAATATGGGCAAGCCTCCAGTGGTAGTTGGTGGAAAGTTACT			2248
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Qy	108	gGluArgArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTrrpAlaGluTyrCy	128
Db	53848	AGAACGAAGAGACGAGGTTCCGATGTCAGAGAAGTACAAGGAGATATGGCAGAGATCT	53789
Qy	128	sLysLeuValProTrrpArgIleLeuProTyrValTyr	140
Db	53788	TAGACTTGTCCCTGGGAATACTTCTTATGTTAT	53752
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JOURNAL			
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ORIGIN			
Alignment Scores:			

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 6587)
AUTHORS Jang, J.-C. and Sheen, J.
TITLE Plant sterol reductases and uses thereof
JOURNAL Patent: US 6639130-A 3 28-OCT-2003;
FEATURES
source location/Qualifiers
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/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
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Score: 496.00 Matches: 107
Percent Similarity: 44.49% Conservative: 14
Best Local Similarity: 39.34% Mismatches: 14
Query Match: 65.70% Indels: 137
DB: 6 Gaps: 3

US-10-069-427-6 (1-140) x AR427912 (1-6587)

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Qy 25 Y----- 25
Db 5421 TAAGTTCTGAGACATGGGGTATTTTCCATCTTACATATCTACACTAAGAAACCCACTA 5480
Qy 26 -----TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLy 40
Db 5481 TTTCTTCTTTGGCAGGTACATGGTTTTCGAGGAGCTACAAACAAACATATCTTTAA 5540
Qy 40 sLysAspProLysAlaProIleTrpGlyLysProProLysValValGlyLysLeuLe 60
Db 5541 GAAGACCCAAACACCAATATATGGGCAAGCCTCCAGTGTAGTTGGTGGAAAGTTACT 5600
Qy 60 uAlaSerGlyTyr-Trp----- 65
Db 5601 GGTTTCAGGCTATTTGGTATGTTATATTTATCTCTCTGTTCTTGTGTTGTTTCGCCA 5660
Qy 65 ----- 65
Db 5661 TCTCTGTTTGTATGTTTCATCATGCTGGCAATAAGAGTTGAAAGTTCCGCAATGACAC 5720
Qy 66 -----GlyIleAlaArgHisCysAs 72
Db 5721 ATTTCCGATTAAGTGTGTTTGTATATATGACAGGGGAATTCGAAGGCACGTGTA 5780
Qy 72 nTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeuProCysGlyVal----- 89
Db 5781 TTACCTGGCGACTGTGATGCTGCTGCTCTTCCTTCAGTTTGGCATGGGAATAGGTACTC 5840
Qy 89 ----- 89
Db 5841 CTNCTGCTTGAGTTCACTTACAGTACCAAAATCATGTAGAAACTAATACCAATATCNAA 5900
Qy 89 ----- 89
Db 5901 ACGTTCGAAGTTGATTTGGCTGACTTAAGATATTGATCTCTAACCATCATTTGAAAGT 5960
Qy 89 ----- 89
Db 5961 CTAAGCTTTCAAGTTCAATTTCCAAAGCTGTTTTTATGATATTTCTGCTNGTGTATTTCT 6020
Qy 90 -SerSerValValProTyrPheTyrProThrTyrLeuLeuIleLeuValLeuArgG1 109
Db 6021 CAGTTCTCCGGTTCCATATTTTACCGGATATACCTGCTGATACTATTTGATATGGAGAG 6080
Qy 109 uArgArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTrpAlaGluTyrCysLy 129
Db 6081 ACGAAGAGACGAAGTTTCAATGTCAGAGAGTACNAGAGAGATATGGCCAGAGTATCTTAG 6140

Qy 129 sLeuValProTyrPheArgGlyLeuProTyrValTyr 140
Db 6141 ACTTGTCCCTGGAGAAATACCTTCCTTATGTTTAT 6174

Search completed: June 14, 2004, 12:18:11
Job time : 2253.35 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 14, 2004, 14:36:55 ; Search time 9.35167 seconds
(without alignments)
772.871 Million cell updates/sec

Title: US-10-069-427-6
Perfect score: 755
Sequence: 1 PRVRKNKVELSLGLANLC.....REIWAECYKLVPRILPYV 140

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCUTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	638	84.5	145	4 US-09-342-653-4	Sequence 4, Appli
2	602	79.7	368	4 US-08-879-337-1	Sequence 1, Appli
3	419	55.5	81	4 US-09-342-653-6	Sequence 6, Appli
4	366	48.5	418	4 US-09-342-653-7	Sequence 7, Appli
5	355	47.0	68	4 US-09-342-653-2	Sequence 2, Appli
6	347.5	46.0	615	4 US-08-879-337-9	Sequence 9, Appli
7	341.5	45.2	424	4 US-08-879-337-5	Sequence 5, Appli
8	300.5	39.8	419	1 US-08-439-131A-3	Sequence 3, Appli
9	300.5	39.8	419	1 US-08-440-674-2	Sequence 2, Appli
10	300.5	39.8	637	4 US-08-879-337-8	Sequence 8, Appli
11	282.5	33.4	438	1 US-08-439-131A-2	Sequence 2, Appli
12	282.5	33.4	438	1 US-08-440-674-5	Sequence 5, Appli
13	252.5	33.4	438	4 US-08-879-337-4	Sequence 4, Appli
14	250	33.1	450	4 US-09-443-041A-22	Sequence 22, Appl
15	247	32.7	430	4 US-09-443-041A-18	Sequence 18, Appl
16	243.5	32.3	432	4 US-09-443-041A-20	Sequence 20, Appl
17	233	30.9	473	1 US-08-439-131A-4	Sequence 4, Appli
18	233	30.9	473	1 US-08-440-674-3	Sequence 3, Appli
19	233	30.9	473	4 US-08-879-337-7	Sequence 7, Appli
20	211	27.9	430	1 US-08-601-435-2	Sequence 2, Appli
21	211	27.9	430	2 US-08-931-047-2	Sequence 2, Appli
22	211	27.9	430	2 US-08-783-202-2	Sequence 2, Appli
23	211	27.9	430	4 US-09-443-041A-31	Sequence 31, Appl
24	205	27.2	453	4 US-08-879-337-6	Sequence 6, Appli
25	195	25.8	453	1 US-08-439-131A-5	Sequence 5, Appli
26	195	25.8	453	1 US-08-440-674-4	Sequence 4, Appli
27	84	11.1	336	4 US-09-252-991A-20404	Sequence 20404, A

28	81.5	10.8	395	4 US-09-797-464A-2	Sequence 2, Appli
29	72	9.5	400	4 US-09-797-464A-4	Sequence 4, Appli
30	71	9.4	160	4 US-09-797-464A-8	Sequence 8, Appli
31	71	9.4	167	4 US-09-797-464A-6	Sequence 6, Appli
32	71	9.4	348	4 US-09-797-464A-7	Sequence 7, Appli
33	70	9.3	363	4 US-09-797-464A-11	Sequence 11, Appl
34	69.5	9.2	217	4 US-09-107-532A-3702	Sequence 3702, Ap
35	69.5	9.2	310	4 US-09-198-452A-864	Sequence 864, App
36	69	9.1	435	4 US-09-491-577-54	Sequence 54, Appl
37	68.5	9.1	1053	4 US-09-394-272-6	Sequence 6, Appli
38	68.5	9.1	1054	1 US-08-356-354-4	Sequence 4, Appli
39	68.5	9.1	1054	2 US-08-778-656-4	Sequence 4, Appli
40	68	9.0	360	4 US-09-252-991A-26052	Sequence 26052, A
41	67.5	8.9	503	3 US-09-068-195-24	Sequence 24, Appl
42	67.5	8.9	616	4 US-09-275-252A-4	Sequence 4, Appli
43	67.5	8.9	668	4 US-09-252-991A-21541	Sequence 21541, A
44	67.5	8.9	1113	4 US-09-618-425-9	Sequence 9, Appli
45	67.5	8.9	3011	3 US-08-811-566-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-342-653-4
; Sequence 4, Application US/09342653
; Patent No. 6306632
; GENERAL INFORMATION:
; APPLICANT: Caboon, Rebecca E.
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Chromatin Associated Proteins
; FILE REFERENCE: BB-1118
; CURRENT APPLICATION NUMBER: US/09/342,653
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/092,841
; EARLIER FILING DATE: July 14, 1998
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-342-653-4

Query Match 84.5%; Score 638; DB 4; Length 145;
Best Local Similarity 82.4%; Pred. No. 2.4e-69;
Matches 112; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY	5	KNKVELSLGLANLCIFLIGYLVPRGANKOKHVFKDPKAPIWGKPKVGGKLLAGY	64
Db	10	RNKVELSLAAVNVCFIVIGYLVPRGANKOKHFKKPKALIWGKPKLVGGKLLVSGY	69
QY	65	WGIAHCHNYLGDLLALSFLPCGVSSVVPYFYPYLLILLVLRERRDEARCSQKYREIW	124
Db	70	WGIAHCHNYLGDLLALSFLPCGVSSVVPYFYPYLLILLVLRERRDEARCSQKYREIW	129
QY	125	AEYCKLVPRILPYVY	140
Db	130	VEYCKLVPRILPYVY	145

RESULT 2
US-08-879-337-1
; Sequence 1, Application US/08879337B
; Patent No. 6639130
; GENERAL INFORMATION:
; APPLICANT: Jang, Uyan-Chyun
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
; FILE REFERENCE: 00786/338001
; CURRENT APPLICATION NUMBER: US/08/879,337B
; CURRENT FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/022,086

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; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-08-879-337-1

Query Match      79.7%; Score 602; DB 4; Length 368;
Best Local Similarity 79.1%; Pred. No. 1.7e-64;
Matches 106; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY      6 NKVELSLGLANICIFLIGLVFRGANKQKHVFKDPKAPIWGKPPKVVGGKLLASGYW 65
DB      235 NKVELTPAIVNCLVFLIGYVFRGANKQKHIFKNPKPTIWGKPPVVGKLLVSGTW 294

QY      66 GIAHCHNYLGDLLALSFSLPCGVSSVVPYFYPTYLILVLRRERDEARCSQKYREIWA 125
DB      295 GIAHCHNYLGDMLALSFSLPCGISTSPVPYFYPTIYLILVRRERDEVRCAEKYKEIWA 354

QY      126 EYCKLVPRILPVY 139
DB      355 EYELVPRILPVY 368

RESULT 3
US-09-342-653-6
; Sequence 6, Application US/09342653
; Patent No. 6306632
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Chromatin Associated Proteins
; FILE REFERENCE: BB-1118
; CURRENT APPLICATION NUMBER: US/09/342,653
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/092,841
; EARLIER FILING DATE: July 14, 1998
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-09-342-653-6

Query Match      55.5%; Score 419; DB 4; Length 81;
Best Local Similarity 90.1%; Pred. No. 3.4e-43;
Matches 73; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      60 LAGYWGIAHCHNYLGDLLALSFSLPCGVSSVVPYFYPTYLILVLRRERDEARCSOK 119
DB      1 LVSGYWGIAHCHNYLGDLLALSFSLPCGASSVVPYFYPTYLILVRRERDEARCSOK 60

QY      120 YREIWAECYCKLVPRILPVY 140
DB      61 YKDIWAECYCKLVPRILPVY 81

RESULT 4
US-09-342-653-7
; Sequence 7, Application US/09342653
; Patent No. 6306632
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Chromatin Associated Proteins
; FILE REFERENCE: BB-1118
; CURRENT APPLICATION NUMBER: US/09/342,653
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/092,841
; EARLIER FILING DATE: July 14, 1998

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; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-342-653-7

Query Match      48.5%; Score 366; DB 4; Length 418;
Best Local Similarity 54.8%; Pred. No. 6.8e-35;
Matches 69; Conservative 20; Mismatches 33; Indels 4; Gaps 3;

QY      19 LCIF-LIGYLVFRGANKQKHVFKDPKAP-IWGRP--PKVVGKLLASGYWGIAHCHNYL 74
DB      293 ICLINAIGYIIFRGANSQKNTFRKNPSDPRVAGLETISTATGRKLLVSGWGMVHRHNYL 352

QY      75 GDLLALSFSLPCGVSSVVPYFYPTYLILVLRRERDEARCSQKYREIWAECYCKLVPR 134
DB      353 GDLLALAWSLPCGVSHLLPYFYLLYFTALLVHRERDERQCLOKYGAWQECYCRVPYR 412

QY      135 ILPVYV 140
DB      413 IMPYIY 418

RESULT 5
US-09-342-653-2
; Sequence 2, Application US/09342653
; Patent No. 6306632
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Chromatin Associated Proteins
; FILE REFERENCE: BB-1118
; CURRENT APPLICATION NUMBER: US/09/342,653
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/092,841
; EARLIER FILING DATE: July 14, 1998
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Zea mays
US-09-342-653-2

Query Match      47.0%; Score 355; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.5e-35;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      75 GDLLALSFSLPCGVSSVVPYFYPTYLILVLRRERDEARCSQKYREIWAECYCKLVPR 134
DB      3 GDLLALSFSLPCGVSSVVPYFYPTYLILVLRRERDEARCSQKYREIWAECYCKLVPR 62

QY      135 ILPVYV 140
DB      63 ILPVYV 68

RESULT 6
US-08-879-337-9
; Sequence 9, Application US/08879337B
; Patent No. 6639130
; GENERAL INFORMATION:
; APPLICANT: Jang, Jyan-Chyun
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
; FILE REFERENCE: 00786/338001
; CURRENT APPLICATION NUMBER: US/08/879,337B
; CURRENT FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/022,086
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 24

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/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 615
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-08-879-337-9

Query Match      46.0%; Score 347.5; DB 4; Length 615;
Best Local Similarity 48.5%; Pred. No. 1.9e-33;
Matches 66; Conservative 22; Mismatches 31; Indels 17; Gaps 3;

QY 16 LANLCIF-LIGYVFRGANKQKHVKPKAPINGKPKVW-----GGKLIASG 64
DB 486 MASLIIVLKUCGVIFRGANSQKNAFKNP-----SDPKLAHLKTIHTSSGKNLLVSGW 539
QY 65 WGAHCHNYLGDLLALLSFLPCGVSSVVPFYFTYLLILLVLRERDEARCSQKYREIW 124
DB 540 WGFVRHPNYLGDLLALAWSLPCGFNHILPFYFIYFTMLLVHREARDEVHCKKYGVAM 599
QY 125 AEYCKLVPRILPYVY 140
DB 600 EKYCQVPIPIFYIY 615

RESULT 7
US-08-879-337-5
/ Sequence 5, Application US/08879337B
/ Patent No. 6639130
/ GENERAL INFORMATION:
/ APPLICANT: Jiang, Jyan-Chyun
/ APPLICANT: Sheen, Jen
/ TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
/ FILE REFERENCE: 00786/338001
/ CURRENT APPLICATION NUMBER: US/08/879,337B
/ CURRENT FILING DATE: 1997-06-20
/ EARLIER APPLICATION NUMBER: 607022,086
/ EARLIER FILING DATE: 1996-06-21
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 5
/ LENGTH: 424
/ TYPE: PRT
/ ORGANISM: Schizosaccharomyces pombe
US-08-879-337-5

Query Match      45.2%; Score 341.5; DB 4; Length 424;
Best Local Similarity 48.9%; Pred. No. 6.4e-33;
Matches 67; Conservative 22; Mismatches 43; Indels 5; Gaps 2;

QY 8 VELSLSLANLCIFLIGYLVFRGANKQKHVKPKAPINGKPKVW----GGKLIASG 63
DB 289 VDLGLVKTALILCLQFLGYIFRGANGQKRNFRSNPNPKL-KHLKFIQTKGTLLTSG 347
QY 64 YWGIARHCNYLGDLLALLSFLPCGVSSVVPFYFTYLLILLVLRERDEARCSQKYREI 123
DB 348 WWMGARHINFGDWINAWANCLPAGFGSP:PYFYVAYFGVLLVHRNARDHDKCRVYKGD 407
QY 124 WAECYCKLVPRILPYVY 140
DB 408 WEKYCKAVKYLPIPYVY 424

RESULT 8
US-08-439-131A-3
/ Sequence 3, Application US/08439131A
/ Patent No. 5512472
/ GENERAL INFORMATION:
/ APPLICANT: Lai, Margaret H. K.
/ APPLICANT: Bard, Martin
/ APPLICANT: Kirsch, Donald R.
/ TITLE OF INVENTION: A DNA Sequence Encoding Sterol Delta
/ Patent No. 5512472
/ TITLE OF INVENTION: Reductase

/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ STREET: One Cyanamid Plaza
/ CITY: Wayne
/ STATE: New Jersey
/ COUNTRY: U.S.A.
/ ZIP: 07470
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA: US/08/439,131A
/ APPLICATION NUMBER: US/08/439,131A
/ FILING DATE: 11-MAY-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/107,347
/ FILING DATE: 16-AUG-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Gordon, Alan M.
/ REGISTRATION NUMBER: 30,637
/ REFERENCE/DOCKET NUMBER: 854-012 (32,141)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-831-3244
/ TELEFAX: 201-831-3305
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 419 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ PUBLICATION INFORMATION:
/ AUTHORS: Worman, H. J.
/ AUTHORS: Evans, C. D.
/ AUTHORS: Blobel, G.
/ TITLE: The Lamin B Receptor of the Nuclear Envelope
/ JOURNAL: J. Cell Biol.
/ VOLUME: 111
/ PAGES: 1535-1542
/ DATE: 1990
/ RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 190 TO 608
US-08-439-131A-3

Query Match      39.8%; Score 300.5; DB 1; Length 419;
Best Local Similarity 48.7%; Pred. No. 5.7e-28;
Matches 55; Conservative 18; Mismatches 37; Indels 3; Gaps 1;

QY 24 IGYLVFRGANKQKHVKFKK---DPKAPIWGKPKPKVVGKLLASGYWGIARHCNYLGDLLA 80
DB 300 IGYVIFRSANSQKNFRNPADPKLSYLKVIPTATGKLLVTGMWGFVRHPNYLGDIIA 359
QY 81 LFSFLPCGVSSVVPFYFTYLLILLVLRERDEARCSQKYREIWAECYCKLVW 133
DB 360 LAWSLPCGFNHILPFYFIYFICLLVHREARDEHCKKYGLAWERYCORVBY 412

RESULT 9
US-08-440-674-2
/ Sequence 2, Application US/08440674
/ Patent No. 5525496
/ GENERAL INFORMATION:
/ APPLICANT: Margaret H. Lai
/ TITLE OF INVENTION: A DNA Sequence Encoding Sterol
/ Patent No. 5525496
/ TITLE OF INVENTION: 14
/ TITLE OF INVENTION: Reductase
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: American Cyanamid Company
```

STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: USA
ZIP: 07470
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,674
FILING DATE: May 15, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,347
FILING DATE: August 16, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Alan M. Gordon
REGISTRATION NUMBER: 30637
REFERENCE/DOCKET NUMBER: 854-P0012 Div (32,141)
TELEPHONE: 201-831-3244
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: polypeptide
FEATURE:
NAME/KEY: chicken
NAME/KEY: nuclear lamin B receptor
PUBLICATION INFORMATION:
AUTHORS: H.J. Worman, C.D. Evans, and G.
AUTHORS: Blobel
TITLE: (excerpt): The Lamin B Receptor of the
TITLE: Nuclear Envelope Inner Membrane
JOURNAL: Journal of Cell Biology
VOLUME: 111
PAGES: 1535-1542
PAGES: Sequence set out in Figure 5, page 1539
Patent No. 5525496
DATE: 1990
RELEVANT RESIDUES IN SEQ ID NO: 190 to 608
US-08-440-674-2
Query Match 39.8%; Score 300.5; DB 1; Length 419;
Best Local Similarity 48.7%; Pred. No. 5.7e-28;
Matches 55; Conservative 18; Mismatches 37; Indels 3; Gaps 1;
QY 24 IGYLVFRGANKQKHFVK---DPKAPIWGKPKVVGKLLASGYWGIAHCHNYLGLLLA 80
Db 300 IGYIFRSANSQKNFRNPADPKLSYLVPTATGKGLLVGTGWGFRHFNHNLGDIIVA 359
QY 81 LSFSLPCGVSSVVPYFYPTVLLILLVLRERDEARCSQKYREIWAECYKLVFW 133
Db 360 LAWSLPCGFNHILPYFYVYFICLLVHREARDEHCKKCYGLAWERYCQVVPY 412
RESULT 10
US-08-879-337-8
Sequence 8, Application US/08879337B
Patent No. 6639130
GENERAL INFORMATION:
APPLICANT: Jang, Jvan-Chyun
APPLICANT: Sheen, Jen
TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
FILE REFERENCE: 00786/338001
CURRENT APPLICATION NUMBER: US/08/879,337B
CURRENT FILING DATE: 1997-06-20

EARLIER APPLICATION NUMBER: 60/022,086
EARLIER FILING DATE: 1996-06-21
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 637
TYPE: PRT
ORGANISM: Gallus domesticus
US-08-879-337-8
Query Match 39.8%; Score 300.5; DB 4; Length 637;
Best Local Similarity 48.7%; Pred. No. 9.6e-28;
Matches 55; Conservative 18; Mismatches 37; Indels 3; Gaps 1;
QY 24 IGYLVFRGANKQKHFVK---DPKAPIWGKPKVVGKLLASGYWGIAHCHNYLGLLLA 80
Db 489 IGYIFRSANSQKNFRNPADPKLSYLVPTATGKGLLVGTGWGFRHFNHNLGDIIVA 548
QY 81 LSFSLPCGVSSVVPYFYPTVLLILLVLRERDEARCSQKYREIWAECYKLVFW 133
Db 549 LAWSLPCGFNHILPYFYVYFICLLVHREARDEHCKKCYGLAWERYCQVVPY 601
RESULT 11
US-08-439-131A-2
Sequence 2, Application US/08439131A
Patent No. 5512472
GENERAL INFORMATION:
APPLICANT: Lai, Margaret H. K.
APPLICANT: Bard, Martin
APPLICANT: Kirsch, Donald R.
TITLE OF INVENTION: A DNA Sequence Encoding Sterol Delta
Patent No. 5512472
TITLE OF INVENTION: Reductase
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07470
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,131A
FILING DATE: 11-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,347
FILING DATE: 16-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Alan M.
REGISTRATION NUMBER: 30,637
REFERENCE/DOCKET NUMBER: 854-012 (32,141)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3244
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-439-131A-2
Query Match 33.4%; Score 252.5; DB 1; Length 438;
Best Local Similarity 38.1%; Pred. No. 3.8e-22;
Matches 53; Conservative 25; Mismatches 48; Indels 13; Gaps 2;

Best Local Similarity 37.3%; Pred. No. 7.9e-22;
 Matches 53; Conservative 31; Mismatches 38; Indels 20; Gaps 6;
 Qy 12 LLGLANLCIFLIGYLVFGANKQKHVFKK-DPKAPIWGK-PPKVVG-----GK 58
 Db 316 LLAGM--LCIV-INY-----DCDRQREFRRTNGKCSWGKAPSKIIVASYQTNGETKSSL 368
 Qy 59 LLASGYGIARHCNLYGDLILLALSFLPCGVSSVVPYFYPTLLILLVLRERDEARCSQ 118
 Db 369 LLTSGWGLSRHFRHYVPEILSAFFWTPALFNFHFLPYFYVIFLTLILFORAKRDDRCSS 428
 Qy 119 KYREIWAECYKLVFWRLPYVY 140
 Db 429 KYGIWKIYCNKVPFVPGIY 450

RESULT 15

US-09-443-041A-18
 ; Sequence 18' Application US/09443041A
 ; Patent No. 6465717
 ; GENERAL INFORMATION:
 ; APPLICANT: Famodu, Omolayo O.
 ; APPLICANT: Orozco, Buddy
 ; APPLICANT: Rafalski, Antoni
 ; APPLICANT: Shen, Jennie
 ; TITLE OF INVENTION: Sterol Metabolism Enzymes
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/443,041A
 ; CURRENT FILING DATE: 1999-11-18
 ; PRIOR APPLICATION NUMBER: 60/109,283
 ; PRIOR FILING DATE: 1998-11-20
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 18
 ; LENGTH: 430
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 US-09-443-041A-18

Query Match 32.7%; Score 247; DB 4; Length 430;

Best Local Similarity 38.0%; Pred. No. 1.7e-21;
 Matches 54; Conservative 28; Mismatches 40; Indels 20; Gaps 6;
 Qy 12 LLGLANLCIFLIGYLVFGANKQKHVFKK-DPKAPIWGK-PPKVV-----GK 58
 Db 296 LLAGI--LCIV-INY-----DCDRQREFRRTNGKCSWGKAPSKIIVASYQTNGETKSSL 348
 Qy 59 LLASGYGIARHCNLYGDLILLALSFLPCGVSSVVPYFYPTLLILLVLRERDEARCSQ 118
 Db 349 LLTSGWGLSRHFRHYVPEILSAFFWTPALFNFHFLPYFYVIFLTLILFORAKRDDRCSS 408
 Qy 119 KYREIWAECYKLVFWRLPYVY 140
 Db 409 KYGIWKIYCNKVPFVPGIY 430

Search completed: June 14, 2004, 14:42:11
 Job time : 10.3517 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 14, 2004, 14:31:29 ; Search time 28.6051 Seconds
(without alignments)
1382.853 Million cell updates/sec

Title: US-10-069-427-6
Perfect score: 755
Sequence: 1 PRYKKNKVELSLSLGLNLC.....REIWAECYKLVPRILPYVY 140

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
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2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	755	100.0	140	4	AAB20380 Soybean s
2	627	83.0	374	4	AAB20379 Corn ster
3	621	82.3	369	4	AAB20381 Soybean s
4	610	80.8	230	3	AAG17153 Arabidops
5	610	80.8	365	3	AAG17152 Arabidops
6	610	80.8	369	3	AAG17151 Arabidops
7	609	80.7	230	3	AAG38708 Arabidops
8	609	80.7	365	3	AAG38707 Arabidops
9	609	80.7	369	2	AAW41576 Arabidops
10	609	80.7	369	3	AAG38706 Arabidops
11	347.5	46.0	615	5	AAU84347 Protein L
12	319.5	42.3	280	4	AAB60759 Gene 13 r
13	319.5	42.3	280	4	AAB60760 Gene 13 r
14	319.5	42.3	475	2	AAU29333 Human sec
15	319.5	42.3	475	2	AAW93573 Human Del
16	319.5	42.3	475	2	AAW93572 Human Del
17	319.5	42.3	475	4	AAU39059 Human sec
18	319.5	42.3	475	5	ABU55768 Human pol
19	319.5	42.3	475	6	ABU89736 Protein d
20	314.5	41.7	471	7	ADU54467 Rat Prote
21	314.5	41.7	471	7	ADU54463 Rat Prote
22	314.5	41.7	471	7	ADU54469 Rat Prote
23	314.5	41.7	471	7	ADU54465 Rat Prote
24	299.5	39.7	448	5	ABP73823 Candida a
25	281	37.2	497	6	ABJ26153 Aspergill

ALIGNMENTS

RESULT 1
AAB20380
ID AAB20380 standard; protein; 140 AA.
XX
AC AAB20380;
XX

DT 11-JUN-2001 (first entry)
XX
DE Soybean sterol delta-14 reductase polypeptide.
XX

KW Soybean; sterol delta-14 reductase; transgenic plant; herbicide;
KW fungicide.
XX

OS Glycine max.
XX

PN WO200123539-A2.
XX

PD 05-APR-2001.
XX

PF 27-SEP-2000; 2000WO-US026442.
XX

PR 30-SEP-1999; 99US-0156820P.
XX

XX (DUPO) DU PONT DE NEMOURS & CO E I.
PA

PI Famodu OO, Kinney AJ;
XX

DR WPI; 2001-266146/27.
XX

DR N-PSDB; AAF30676.
XX

PT Novel gene encoding sterol delta-14 reductase useful for transgenic plant
production with altered sterol delta-14 reductase.
XX

PS Claim 1(b); Page 38; 45pp; English.
XX

CC The present sequence is that of a soybean sterol delta-14 reductase
polypeptide, as deduced from a partial coding sequence from the full
insert sequence of a clone (see AAF30676) isolated from a cyst nematode-
infected soybean 8-day-old root cDNA library. The predicted polypeptide
shows amino acid sequence homology to Arabidopsis thaliana and Ascorbous
immensus sterol delta-14 reductases. The invention relates to sterol
delta-14 reductase polynucleotides and polypeptides and to transgenic
plants comprising the polynucleotides. It also relates to the
construction of a chimeric gene encoding all or a portion of the sterol
delta-14 reductase, in sense or antisense orientation, where expression
of the chimeric gene results in production of altered levels of the
enzyme in a transformed host cell. The availability of plant sterol delta
-14 reductase genes will provide a means of altering sterol production
CC

CC and/or composition of plants, to identify compounds that may be useful as
 CC novel herbicides and fungicides, and to identify mutants of these genes
 CC that are resistant to these herbicides and will enable the production of
 CC herbicide-resistant crops

XX SQ Sequence 140 AA;
 Query Match 100.0%; Score 755; DB 4; Length 140;
 Best Local Similarity 100.0%; Pred. No. 5.5e-84; Indels 0; Gaps 0;
 Matches 140; Conservative 0; Mismatches 0;
 QY 1 PRVRKNVELSLGLANLCIFLIGYLVFRGANKQKHVFKDKAPWGPVKVGGKLL 60
 DB 1 PRVRKNVELSLGLANLCIFLIGYLVFRGANKQKHVFKDKAPWGPVKVGGKLL 60
 QY 61 ASGWGVIARHCNLYGLDILLALSFSLPCGVSVVPYFYPTVLLLVLRERRDEARCSQY 120
 DB 61 ASGWGVIARHCNLYGLDILLALSFSLPCGVSVVPYFYPTVLLLVLRERRDEARCSQY 120
 QY 121 REIWAECYKLVPRILPYVY 140
 DB 121 REIWAECYKLVPRILPYVY 140

RESULT 2
 AAB20379
 ID AAB20379 standard; protein; 374 AA.
 AC AAB20379;
 DT 11-JUN-2001 (first entry)
 DE Corn sterol delta-14 reductase.
 DE Corn; maize; sterol delta-14 reductase; transgenic plant; herbicide;
 KW fungicide.
 OS Zea mays.
 OS WO200123539-A2.
 PN 05-APR-2001.
 PD 27-SEP-2000; 2000WO-US026442.
 PF 30-SEP-1999; 99US-0156820P.
 PR (DUPO) DU PONT DE NEMOURS & CO E I.
 PA Famodu OO, Kinney AJ;
 PI WPI; 2001-266146/27.
 DR N-PSDB; AAF30675.
 PT Novel gene encoding sterol delta-14 reductase useful for transgenic plant
 PT production with altered sterol delta-14 reductase.
 PS Claim 1(b); Page 36-38; 45pp; English.

CC The present sequence is that of corn sterol delta-14 reductase, as
 CC deduced from the full insert sequence of a clone (see AAF30675) isolated
 CC from an ECB infested 99 whorl section cDNA library. The predicted protein
 CC shows amino acid sequence homology to Arabidopsis thaliana and Ascomolus
 CC immersus sterol delta-14 reductases. The invention relates to sterol
 CC delta-14 reductase polynucleotides and polypeptides and to transgenic
 CC plants comprising the polynucleotides. It also relates to the
 CC construction of a chimeric gene encoding all or a portion of the sterol
 CC delta-14 reductase, in sense or antisense orientation, where expression
 CC of the chimeric gene results in production of altered levels of the
 CC enzyme in a transformed host cell. The availability of plant sterol delta
 CC -14 reductase genes will provide a means of altering sterol production
 CC and/or composition of plants, to identify compounds that may be useful as
 CC novel herbicides and fungicides, and to identify mutants of these genes

CC that are resistant to these herbicides and will enable the production of
 CC herbicide-resistant crops
 XX SQ Sequence 374 AA;

Query Match 83.0%; Score 627; DB 4; Length 374;
 Best Local Similarity 83.0%; Pred. No. 9.4e-68;
 Matches 112; Conservative 13; Mismatches 10; Indels 0; Gaps 0;
 QY 6 NKVELSLGLANLCIFLIGYLVFRGANKQKHVFKDKAPWGPVKVGGKLLASGYW 65
 DB 240 NSVELTPAATVANCVFVLIGYLVFRGANKQKHVFKDKAPWGPVKVGGKLLASGYW 299
 QY 66 GIARHCNLYGLDILLALSFSLPCGVSVVPYFYPTVLLLVLRERRDEARCSQYRIWA 125
 DB 300 GIARHCNLYGLDILLALSFSLPCGVSVVPYFYPTVLLLVLRERRDEARCSQYRIWA 359
 QY 126 EYKLVPRILPYVY 140
 DB 360 EYKLVPRILPYVY 374

RESULT 3
 AAB20381
 ID AAB20381 standard; protein; 369 AA.
 AC AAB20381;
 DT 11-JUN-2001 (first entry)
 DE Soybean sterol delta-14 reductase.
 DE Soybean; sterol delta-14 reductase; transgenic plant; herbicide;
 KW fungicide.
 OS Glycine max.
 OS WO200123539-A2.
 PN 05-APR-2001.
 PD 27-SEP-2000; 2000WO-US026442.
 PF 30-SEP-1999; 99US-0156820P.
 PR (DUPO) DU PONT DE NEMOURS & CO E I.
 PA Famodu OO, Kinney AJ;
 PI WPI; 2001-266146/27.
 DR N-PSDB; AAF30677.
 PT Novel gene encoding sterol delta-14 reductase useful for transgenic plant
 PT production with altered sterol delta-14 reductase.
 PS Claim 1(b); Page 39-40; 45pp; English.

CC The present sequence is that of soybean sterol delta-14 reductase, as
 CC deduced from a full-length coding sequence from the full insert sequence
 CC of a clone (see AAF30677) isolated from a soybean shoot meristem cDNA
 CC library. The predicted protein shows amino acid sequence homology to
 CC Arabidopsis thaliana and Ascomolus immersus sterol delta-14 reductases.
 CC The invention relates to sterol delta-14 reductase polynucleotides and
 CC polypeptides and to transgenic plants comprising the polynucleotides. It
 CC also relates to the construction of a chimeric gene encoding all or a
 CC portion of the sterol delta-14 reductase, in sense or antisense
 CC orientation, where expression of the chimeric gene results in production
 CC of altered levels of the enzyme in a transformed host cell. The
 CC availability of plant sterol delta-14 reductase genes will provide a
 CC means of altering sterol production and/or composition of plants, to
 CC identify compounds that may be useful as novel herbicides and fungicides,
 CC and to identify mutants of these genes that are resistant to these
 CC herbicides and will enable the production of herbicide-resistant crops


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XX Sequence 369 AA;
SQ
Query Match      82.3%; Score 621; DB 4; Length 369;
Best Local Similarity 82.2%; Pred. No. 5e-67;
Matches 111; Conservative 13; Mismatches 11; Indels 0; Gaps 0;
QY      6 NKVELSLSLGLANLCLFLIGYLVFRGANKOKHVFKDKPKAPIWGKPPKVVGKLLASGYW 65
DB      235 NSVELTPAAIVANCFVFLIGYLVFRGANKOKHVFKDKPKAPIWGKPPKVVGKLLASGYW 294
QY      66 GIARHCNVLGDLMLALSFSLPCGVSSVVPYFYPTYLILVLRRDEARCSOKYREIWA 125
DB      295 GIARHCNVLGDLMLALSFSLPCGVSSVVPYFYPTYLILVLRRDEARCSOKYREIWA 354
QY      126 EYKLVPEWRLPYVY 140
DB      355 EYKLVPEWRLPYVY 369

RESULT 4
AAG17153
ID ARG17153 standard; protein; 230 AA.
XX
AC AAG17153;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 18066.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
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Qy 66 GIARHCNVLGDLMLALSFSLPCGVSSVVPYFYPTIYLLILVLRRERDEARCSOKYREIWA 125
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
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XX
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PD 06-SEP-2000.
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PR	14-MAY-1999;			PR	23-JUL-1999;	99US-0145218P.
PR	14-MAY-1999;			PR	23-JUL-1999;	99US-0145224P.
PR	14-MAY-1999;			PR	26-JUL-1999;	99US-0145276P.
PR	14-MAY-1999;			PR	27-JUL-1999;	99US-0145913P.
PR	14-MAY-1999;			PR	27-JUL-1999;	99US-0145918P.

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PR 22-OCT-1999; 99US-0160988P.
PR 23-OCT-1999; 99US-0161404P.

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PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 80.7%; Score 609; DB 3; Length 369;
Best Local Similarity 79.3%; Pred. No. 1.5e-65;
Matches 107; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 6 NKVELSLGSLANLCIFLIGYLVFRGANKQKHVPKDKPAPIMGKPKPVVGGKLLASGYW 65
| | | | | : : : | | | | | : | | | | | : | | | | | : | | | | |
Db 235 NKVELTPVAIVVNCVFLIGYLVFRGANKQKHVPKDKPAPIMGKPKPVVGGKLLVSGYW 294
| | | | | : : : | | | | | : | | | | | : | | | | | : | | | | |

QY 66 GIARHCNVLGDLALSFSLPCGVSSVVPYFPTYLILVLRRERDEARCSOKYREIWA 125
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 295 GIARHCNVLGDLALSFSLPCGVSSVVPYFPTYLILVLRRERDEARCSOKYREIWA 354
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 126 EYKLVPRILPYVY 140
| | | | | : | | | | |
Db 355 EYKLVPRILPYVY 369
| | | | | : | | | | |

RESULT 11
AAU84347
ID AAU84347 standard; protein; 615 AA.
XX
AC AAU84347;
XX
DT 08-MAY-2002 (first entry)
XX
DE Protein LBR differentially expressed in breast cancer tissue.
XX
KW Human; diagnosis of breast cancer; endometrial cancer; breast tumour;
KW MAI; mitotic activity index; cytostatic.
XX
OS Homo sapiens.
XX
FN WO200210436-A2.
XX
PD 07-FEB-2002.
XX
PF 27-JUL-2001; 2001WO-US023642.
XX
PR 28-JUL-2000; 2000US-0222093P.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
PA (BAAK/) BAAK J.
XX
Baak J, Mutter GL;
XX
WPI; 2002-180084/23.
DR N-PSDB; ABK35567.
XX
Diagnosing breast cancer comprises determining expression of nucleic acid
molecules or expression products that are differentially expressed in
normal and malignant tissue.
XX
Claim 37; Page 183-185; 219pp; English.
XX
The present invention relates to a method for diagnosing breast cancer in
a subject suspected of having endometrial cancer. The method comprises
determining the expression of a set of human genes or expression products
in an endometrial sample suspected of being cancerous. The human genes of
the invention are differentially expressed in breast tumours
characterised as high or low MAI (mitotic activity index). These sets of
genes can be used to discriminate between high and low MAI breast
tumours. The invention also provides DNA and protein microarrays for
analysing the expression of the human genes and their protein products.
CC
```

CC The methods and arrays are useful for the diagnosis and prognosis of
 CC endometrial cancer, selecting and monitoring treatment regimes, and
 CC identification of compounds useful for the treatment of endometrial
 CC cancer. AAU84311-AAU84361 represent the human proteins of the invention
 CC that are differentially expressed in breast cancer tissue
 XX
 SQ Sequence 615 AA;

Query Match 46.0%; Score 347.5; DB 5; Length 615;
 Best Local Similarity 48.5%; Pred. No. 3e-33;
 Matches 66; Conservative 22; Mismatches 31; Indels 17; Gaps 3;
 QY 16 LANLCIF--LIGLVFRGANKQKHVFKKDKPAPIWGKPKVW-----GKKLASGY 64
 DB 486 MASLIIVLKGVIFRGANSQNAFKNP-----SDPKLAHLKTIHTSSGKLLVSGW 539
 QY 65 WGIARHCNYLGDLALLSFLPCGVSSVVPFYPTYLILLVLRERDEARCSQKYREIW 124
 DB 540 WGFVRHNPYGLDMLALAWSLPCGFNHLFPFYIYFTMLLVHREARDEYHCKKYGVAW 599
 QY 125 AEYCKLVPWRILPVY 140
 DB 600 EKYCQVPYRIFPYIY 615

RESULT 12
 AAB60759
 ID AAB60759 standard; peptide; 280 AA.
 XX
 AC AAB60759;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Gene 13 related peptide #1.
 XX
 KW Secreted protein; gene therapy; vaccine; cancer; leukemia;
 KW autoimmune disease; allergy; inflammation; graft rejection;
 KW hyperproliferation; cardiovascular; infection.
 XX
 OS Homo sapiens.
 XX
 PN WO200076531-A1.
 XX
 PD 21-DEC-2000.
 XX
 PF 01-JUN-2000; 2000WO-US015137.
 XX
 PR 11-JUN-1999; 99US-0138625P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM, Komatsoulis GA;
 XX
 DR WPI; 2001-071148/08.
 XX
 PT Nucleic acids encoding 47 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease
 PT and diabetic retinopathy.
 XX
 PS Disclosure; Page 513-514; 525pp; English.
 XX
 CC The present invention relates to 26 secreted human proteins. The proteins
 CC may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. For example, they
 CC may be used in gene therapy or in vaccines. Typical of diseases which are
 CC potentially treatable are cancers (including leukemia), autoimmune
 CC diseases, allergies, inflammation, graft rejection, hyperproliferation,
 CC cardiovascular diseases (particularly critical limb ischemia and coronary
 CC disease) and any involving abnormal angiogenesis, neurodegeneration
 CC and/or infectious diseases
 XX
 SQ Sequence 280 AA;

Query Match 42.3%; Score 319.5; DB 4; Length 280;
 Best Local Similarity 43.2%; Pred. No. 2.8e-30;
 Matches 63; Conservative 26; Mismatches 44; Indels 13; Gaps 2;
 QY 8 VELSLSLGLANLCIFLIGLVFRGANKQKHVFKK-DPKAPIWGKPKVW----- 55
 DB 135 VOLSTPHAVGVLLGLGVGYIFRVANHQKDLFRRTDGRCLWGKPKVIECSYTSADGQR 194
 QY 56 -GGKLLASGYWGIAHCHNYLGDLALLSFLPCGVSSVVPFYPTYLILLVLRERDEA 114
 DB 195 HSKLLVSGFVGVAHFHFNVDLMSGLAYCLACGGHLLPFYIYIMAILLTHRCLEH 254
 QY 115 RGSQKYREIWAECYCKLVPWRILPVY 140
 DB 255 RCASKYGRDWERYTAAPFYRLPGIF 280
 RESULT 13
 AAB60760
 ID AAB60760 standard; peptide; 280 AA.
 XX
 AC AAB60760;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Gene 13 related peptide #2.
 XX
 KW Secreted protein; gene therapy; vaccine; cancer; leukemia;
 KW autoimmune disease; allergy; inflammation; graft rejection;
 KW hyperproliferation; cardiovascular; infection.
 XX
 OS Homo sapiens.
 XX
 PN WO200076531-A1.
 XX
 PD 21-DEC-2000.
 XX
 PF 01-JUN-2000; 2000WO-US015137.
 XX
 PR 11-JUN-1999; 99US-0138625P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM, Komatsoulis GA;
 XX
 DR WPI; 2001-071148/08.
 XX
 PT Nucleic acids encoding 47 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease
 PT and diabetic retinopathy.
 XX
 PS Disclosure; Page 514-515; 525pp; English.
 XX
 CC The present invention relates to 26 secreted human proteins. The proteins
 CC may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. For example, they
 CC may be used in gene therapy or in vaccines. Typical of diseases which are
 CC potentially treatable are cancers (including leukemia), autoimmune
 CC diseases, allergies, inflammation, graft rejection, hyperproliferation,
 CC cardiovascular diseases (particularly critical limb ischemia and coronary
 CC disease) and any involving abnormal angiogenesis, neurodegeneration
 CC and/or infectious diseases
 XX
 SQ Sequence 280 AA;

Query Match 42.3%; Score 319.5; DB 4; Length 280;
 Best Local Similarity 43.2%; Pred. No. 2.8e-30;
 Matches 63; Conservative 26; Mismatches 44; Indels 13; Gaps 2;
 QY 8 VELSLSLGLANLCIFLIGLVFRGANKQKHVFKK-DPKAPIWGKPKVW----- 55
 DB 135 VOLSTPHAVGVLLGLGVGYIFRVANHQKDLFRRTDGRCLWGKPKVIECSYTSADGQR 194

Qy	56	-CGKLLASGYGIARHONCYLGDLLLSPLPGVSVSVVPEFYPTVLLILLVLRSRDEA	114
Db	390	HHSKLLVSGFGVGRHHNYGVGLMGSLLAYCLACGGHLLPFYIIYMAILLTHRCURDEH	449
Qy	115	RCQKYREIWAECYKLVPRILPYVY	140
Db	450	RCASKYGRDWRERYTAAVPYRLLPGIF	475

RESULT 15	
AAW93573	
ID	AAW93573 standard; protein; 475 AA.
XX	
AC	AAW93573;
XX	
DT	17-JUN-1999 (first entry)
XX	
DE	Human Delta7-sterol reductase protein.
XX	
XX	Human; Delta7-sterol reductase; hereditary; Smith-Lemli-Opitz syndrome;
KW	diagnosis; screening; double bond removal; 7-dehydrocholesterol;
KW	organic polymeric ring; cholesterol.
XX	
OS	Homo sapiens.
XX	
PN	DE19739940-A1.
XX	
PD	18-MAR-1999.
XX	
PF	11-SEP-1997; 97DE-01039940.
XX	
PR	11-SEP-1997; 97DE-01039940.
XX	
PA	(GLOS/) GLOSSMANN H.
XX	
PI	Glossmann H, Moebius F, Fitzky B;
XX	
DR	WPI; 1999-191430/17.
DR	N-PSDB; AAX23387.
XX	
PT	Human Delta7-sterol reductase polypeptide - useful for diagnosis or
PT	treatment of genetic defects e.g. hereditary Smith-Lemli-Opitz syndrome.
XX	
PS	Disclosure: Page 29-30; 62pp; German.

CC can be used to diagnose or collect human data, and it reduces the
CC defects and Delta7-sterol reductase polymorphisms which can be used to
CC replace a defective Delta7-sterol reductase enzyme in humans or other
CC animals. It is also useful to screen for Delta7-sterol reductase
CC inhibitors or to introduce and remove double bonds in synthetic and
CC naturally occurring organic polymeric ring systems (Delta 7-sterol
CC reductase catalyses the conversion of 7-dehydrocholesterol to
CC cholesterol)

QY	8	VEESSESSECECLFLLGIIKIRKRNQXAVICL	8	VEESSESSECECLFLLGIIKIRKRNQXAVICL	8	VEESSESSECECLFLLGIIKIRKRNQXAVICL
		: : : : : : : :		: : : : : : : :		: : : : : : : :
Db	330	VQLSTPHAVGLLGLVGYIFRVANHQDLFFRTGRL	330	VQLSTPHAVGLLGLVGYIFRVANHQDLFFRTGRL	330	VQLSTPHAVGLLGLVGYIFRVANHQDLFFRTGRL
		: : : : : : : :		: : : : : : : :		: : : : : : : :
QY	56	-GGKLLASGYGIAHRCNVLGDLLALSLPCGVS	56	-GGKLLASGYGIAHRCNVLGDLLALSLPCGVS	56	-GGKLLASGYGIAHRCNVLGDLLALSLPCGVS
		: : : : : : : :		: : : : : : : :		: : : : : : : :
Db	390	HHSKLLVSGFVGVARHNYVGDMLSLAYCLACGG	390	HHSKLLVSGFVGVARHNYVGDMLSLAYCLACGG	390	HHSKLLVSGFVGVARHNYVGDMLSLAYCLACGG
		: : : : : : : :		: : : : : : : :		: : : : : : : :
QY	115	RCISKYREINAWBYCKLVPRILPVY	115	RCISKYREINAWBYCKLVPRILPVY	115	RCISKYREINAWBYCKLVPRILPVY
		: : : : : : : :		: : : : : : : :		: : : : : : : :
Db	450	RCASKYGRDWERYTAAPVYRLLPGIF	450	RCASKYGRDWERYTAAPVYRLLPGIF	450	RCASKYGRDWERYTAAPVYRLLPGIF
		: : : : : : : :		: : : : : : : :		: : : : : : : :

Search completed: June 14, 2004, 14:38:48
Job time : 31.6051 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2004, 09:48:07 ; Search time 228.291 Seconds
(without alignments)
2605.220 Million cell updates/sec

Title: US-10-069-427-6
Perfect score: 755
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 337363 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 29Jan04:*
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3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	755	100.0	667	AAF30676	Aaf30676 Soybean s
2	630	83.4	625	ADD17001	Add17001 DNA (Seq)
3	627	83.0	1631	AAF30675	Aaf30675 Corn ster
4	621	82.3	1364	AAF30677	Aaf30677 Soybean s
5	610	80.8	1380	AAF30673	Aac37623 Arabidops
6	609	80.7	1110	AAC45795	Aac45795 Arabidops
7	609	80.7	1429	AAV04237	Aav04237 Arabidops
8	496	65.7	6588	AAV04238	Aav04238 Arabidops

9	356.5	47.2	3714	6	ABX35567	Abk35567 Gene LBR
10	356.5	47.2	3714	6	ABK83864	Abk83864 Human cDN
c 11	321.5	42.6	476	9	ADB56005	ADB56005 Toxicity-
12	319.5	42.3	1896	4	Aaf26559	Aaf26559 DNA encod
13	319.5	42.3	2481	2	AAX90448	Aax90448 Human sec
14	319.5	42.3	2481	2	AAS59277	Aas59277 Human cDN
15	319.5	42.3	2481	6	ABA90946	Abay90946 Human pol
16	319.5	42.3	2652	2	AAx23387	Aax23386 Human Del
17	319.5	42.3	2652	2	AAx23386	Aax23386 Human Del
18	314.5	41.7	2427	9	ADB58439	ADB58439 Toxicity-
19	314.5	41.7	2427	9	ADB53021	ADB53021 Primary r
20	305.5	40.5	1546	6	ABQ54166	Abq54166 Human ova
c 21	302	40.0	458	6	ABN94581	ABn94581 Gene #107
c 22	299.5	39.7	1347	6	ABZ32373	Abz32373 Candida a
c 23	293.5	38.9	428	3	AAA77792	Aaa77792 cDNA enco
c 24	293.5	38.9	428	4	AAI28530	Aai28530 Colon tum
c 25	293.5	38.9	428	7	ABZ32716	Abz32716 Human col
26	281	37.2	1494	7	ABT20861	Abt20861 Aspergill
27	281	37.2	1614	7	ABT20263	Abt20263 Aspergill
28	279	37.0	1875	9	ADD69664	Add69664 Human REM
29	269.5	35.7	3242	7	ABT17853	Abt17853 Aspergill
30	262.5	34.8	1245	7	ABT19041	Abt19041 Aspergill
c 31	252.5	33.4	800	9	ADD16149	Add16149 cDNA (Seq
32	252.5	33.4	2528	2	AAQ89202	Aaq89202 Sterol-de
33	252.5	33.4	2528	2	AAQ89202	Aaq89202 Sterol-de
34	252.5	33.4	2528	2	AAQ89202	Aaq89202 Sterol-de
35	252.5	33.4	2528	2	AAQ89202	Aaq89202 Sterol-de
36	250	33.1	1695	7	ABX15831	Abx15831 cDNA enco
37	247	32.7	1870	7	ABX15829	Abx15829 cDNA enco
c 38	243.5	32.3	1646	6	ABQ85384	Abq85384 Arabidops
39	231	30.6	376	6	ABQ85384	Abq85384 Arabidops
40	225	29.8	588	7	ABX56738	Abx56738 Arabidops
41	225	29.8	1299	6	ABZ14307	Abz14307 Arabidops
42	225	29.8	1336	3	AAc40077	Aac40077 Arabidops
43	225	29.8	1501	3	AAc51344	Aac51344 Arabidops
44	225	29.8	1531	6	ABQ82663	Abq82663 Arabidops
45	211	27.9	1496	2	AAT39358	Aat39358 Arabidops

ALIGNMENTS

RESULT 1
AAF30676
ID AAF30676 standard; cDNA; 667 BP.
XX
AC AAF30676;
XX
DT 11-JUN-2001 (first entry)
XX
DE Soybean sterol delta-14 reductase clone src3c.pk009.cl:fls.
XX
KW Soybean; sterol delta-14 reductase; transgenic plant; herbicide;
KW fungicide; ss.
XX
OS Glycine max.
XX
FH Key Location/Qualifiers
FT CDS 1..423
FT /*tag= a
FT /partial
XX
FN WO200123539-A2.
XX
PD 05-APR-2001.
XX
PF 27-SEP-2000; 2000WO-US026442.
XX
PR 30-SEP-1999; 99US-0156820P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PI Famodu OO, Kinney AJ;
XX

DR WPI; 2001-266146/27.
 DR P-PSDB; AAB20380.
 XX Novel gene encoding sterol delta-14 reductase useful for transgenic plant
 PT production with altered sterol delta-14 reductase.
 XX Claim 7; Page 38; 45pp; English.
 XX The present sequence is that of the full insert sequence of clone
 CC src3c.pk009.cl, which includes a partial coding region for soybean sterol
 CC delta-14 reductase (see AAB20380). The clone was isolated from a cDNA
 CC library prepared from soybean 8-day-old root infected with cyst nematode,
 CC following database homology searches. The predicted polypeptide shows
 CC amino acid sequence homology to Arabidopsis thaliana and Ascorbolus
 CC immersus sterol delta-14 reductases. The invention relates to isolated
 CC polynucleotides encoding sterol delta-14 reductases and to transgenic
 CC plants comprising such polynucleotides. It also relates to the
 CC construction of a chimeric gene encoding all or a portion of the sterol
 CC delta-14 reductase, in sense or antisense orientation, where expression
 CC of the chimeric gene results in production of altered levels of the
 CC enzyme in a transformed host cell. The availability of plant sterol delta
 CC -14 reductase genes will provide a means of altering sterol production
 CC and/or composition of plants, to identify compounds that may be useful as
 CC novel herbicides and fungicides, and to identify mutants of these genes
 CC that are resistant to these herbicides and will enable the production of
 CC herbicide-resistant crops
 XX

SQ Sequence 667 BP; 204 A; 144 C; 161 G; 158 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.38e-85 Length: 667
 Score: 755.00 Matches: 140
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-10-069-427-6 (1-140) x AAF30676 (1-667)

Qy 1 ProArgValArgLysAsnLysValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCys 20
 Db 1 CCAGCGTCGCGGAGAACAAAGTAGAGCTGTCCTTTTGTCTGTAGTAACTTATGC 60
 Qy 21 IlePheLeuIleGlyTyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLys 40
 Db 61 ATCTTTCTTATGCTACCTAGTGTTCGAGGAGCTAACCAAGCAAAACATGTGTTCAAG 120
 Qy 41 LysAspProLysAlaProIleTyrGlyLysProLysValValGlyGlyLysLeuLeu 60
 Db 121 AAGGACCCCAAGCTCTATATGCGGGAACCTCCCAAGATTCTCGGGGAAAGCTACTA 180
 Qy 61 AlaSerGlyTyrTyrGlyValLeuAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAla 80
 Db 181 GCATCTGTTACTGGGCGATCGCAAGGACATGCAATTATCTCGGAGACCTGCTAGCA 240
 Qy 81 LeuSerPheSerLeuProCysGlyValSerValValProTyrPheTyrProThrTyr 100
 Db 241 CTTTCGTTCACTGCTCCCTGCGAGTGAGTTCGCTCCATCTTACCCACGCTAC 300
 Qy 101 LeuLeuIleLeuLeuValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyr 120
 Db 301 CTGCTCATTTCTACTGTGTTTGGGGAAGCGGATGAGCGAGGTGCTCGCAGAGTAC 360
 Qy 121 ArgGluIleTrpAlaGluTyrCysLysLeuValProTrpArgIleLeuProTyrValTyr 140
 Db 361 AGGAGATCTGGGCGAGAGTACTGCAAGCTCGTCCGCTGGAGGATCTGCTTATGTGAC 420
 RESULT 2
 ADD17001
 ID ADD17001 standard; DNA; 625 BP.
 XX
 AC ADD17001;
 XX

DT 15-JAN-2004 (first entry)
 XX DNA (SeqID 1069) that confers an altered visual phenotype in plants.
 DE ds; visual phenotype; plant; architecture; leaf surface; chlorotic;
 KW bleaching; etching; wet leaf; stunting; elongation; texture;
 KW agronomic trait; growth regulation; dwarf variety; insect resistance;
 KW heat stress; transgenic.
 XX Unidentified.
 OS WO2003020741-A1.
 PN 13-MAR-2003.
 XX 30-AUG-2002; 2002WO-US027880.
 PF 31-AUG-2001; 2001US-0316326P.
 PR (DOWC) DOW CHEM CO.
 PA (DOWC) DOW AGROSCIENCES LLC.
 XX Crosley R, Skokut T, Ruegger M, Larrinua I, Shukla V;
 PI WPI; 2003-300858/29.
 DR Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae
 XX sativa, Saccharomyces cerevisiae, and Papaver rhoeas, useful for
 PT conferring altered visual phenotypes in plants.
 PT Claim 1; SEQ ID NO 1069; 517pp; English.
 PS This invention relates to the identification and isolation of novel
 XX nucleic acid molecules that confer altered visual phenotypes in plants.
 CC Specifically, it refers to modifications of plant architecture and/or
 CC leaf surface features in plants, such as chlorotic, bleaching, etching,
 CC wet leaf, stunting, elongation and texture phenotypes, which are thought
 CC will be agronomic traits beneficial to the farmer. As such, these novel
 CC phenotypes can affect growth regulation i.e. useful for creating dwarf
 CC varieties, exhibit resistance to insects or heat stress, confer changes
 CC in pigment content such that plants have enhanced vitamin production or
 CC delayed senescence and also for example produce plants that control the
 CC production of ethylene. Furthermore, the present invention comprises
 CC generating transgenic plants, as well as reproducibly altering the visual
 CC phenotype of plant seeds, plant tissues and plant cells containing the
 CC polynucleotides described herein. This polynucleotide is a homologue of a
 CC DNA sequence that confers an altered visual phenotype when expressed in
 CC plants, the method of the invention.
 XX Sequence 625 BP; 165 A; 117 C; 149 G; 194 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.04e-70 Length: 625
 Score: 630.00 Matches: 111
 Percent Similarity: 92.59% Conservatives: 14
 Best Local Similarity: 82.22% Mismatches: 10
 Query Match: 83.44% Indels: 0
 DB: 9 Gaps: 0

US-10-069-427-6 (1-140) x ADD17001 (1-625)

Qy 6 AsnLysValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIleGly 25
 Db 209 AACAAAGTGGAACTAACCAAGCAGCAGTAAATCCCAATTCCTCGCTTCTTATGGG 269
 Qy 26 TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysAspProLysAla 45
 Db 269 TACTTAGTTCACAGGTGCAACACAGCAGCATATGTTTAAAGAAATCCCAAGCA 328
 Qy 46 ProIleTrpGlyLysProLysValValGlyLysLeuAlaSerGlyTyrTyr 65
 Db 329 CCCATATGGGGTAAGCTCCCAAGATTATTATGGGGGAAGTTCCTCGCTTCTGCTATGG 389

QY 66 GlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeu 85
 DB 389 GGCATTGCTCGACACTGAATTACCTTGGAGATTGTTGGCATTTGTCATTAGTTG 448
 QY 86 ProCysGlyValSerValProTyrPheTyrProTyrLeuLeuLeuLeu 105
 DB 449 CTTGTGGGATAAGTCCGGGTCCCATCTTTTACCCCATATATCTTCTTATCTGCTA 508
 QY 106 ValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTyrPala 125
 DB 509 ATATGGAGGGAGAGAGAGATGAAGCTCGATGTCAGAGAGATGAAGAGCTGGGACA 568
 QY 126 GluTyrCysLysLeuValProTyrPheTyrPheTyrValTyr 140
 DB 569 GAATACCGTAAACTTGTCTCTGGAGGATATACCGTACGTTTAC 613

RESULT 3

AAF30675
 ID AAF30675 standard; cDNA; 1631 BP.

XX AC AAF30675;
 XX 11-JUN-2001 (first entry)
 XX Corn sterol delta-14 reductase clone p0097.cqraus7ra.fis.
 DE Corn; maize; sterol delta-14 reductase; transgenic plant; herbicide;
 KW fungicide; ss.
 KW Zea mays.

XX Key Location/Qualifiers
 FT CDS 74..1198
 FT /*tag= a

XX WO200123539-A2.

XX 05-APR-2001.

XX 27-SEP-2000; 2000WO-US026442.

XX 30-SEP-1999; 99US-0156820P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Famodu OO, Kinney AJ;

XX WPI; 2001-266146/27.

XX P-PSDB; AAB20379.

XX Novel gene encoding sterol delta-14 reductase useful for transgenic plant
 production with altered sterol delta-14 reductase.

XX Claim 7; Page 36; 45pp; English.

XX The present sequence is that of the full-insert sequence of clone
 CC p0097.cqraus7ra.fis, coding for corn sterol delta-14 reductase (see
 CC AAB20379). The clone was isolated from a cDNA library prepared from corn
 CC V9 whorl section + ECBI, following database homology searches. The
 CC predicted polypeptide shows amino acid sequence homology to Arabidopsis
 CC thaliana and Ascorobolus immersus sterol delta-14 reductases. The invention
 CC relates to isolated polynucleotides encoding sterol delta-14 reductases
 CC and to transgenic plants comprising such polynucleotides. It also relates
 CC to the construction of a chimeric gene encoding all or a portion of the
 CC sterol delta-14 reductase, in sense or antisense orientation, where
 CC expression of the chimeric gene results in production of altered levels
 CC of the enzyme in a transformed host cell. The availability of plant
 CC sterol delta-14 reductase genes will provide a means of altering sterol
 CC production and/or composition of plants, to identify compounds that may
 CC be useful as novel herbicides and fungicides, and to identify mutants of
 CC these genes that are resistant to these herbicides and will enable the
 CC production of herbicide-resistant crops

SQ Sequence 1631 BP; 392 A; 330 C; 353 G; 556 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 7,448-69 Length: 1631
 Score: 627.00 Matches: 112
 Percent Similarity: 92.59% Conservative: 13
 Best Local Similarity: 82.96% Mismatches: 10
 Query Match: 83.05% Indels: 0
 DB: 4 Gaps: 0

US-10-069-427-6 (1-140) x AAF30675 (1-1631)

QY 6 AsnLysValGluLeuSerLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIleGly 25
 DB 791 AACAGTGTGGAGTTAAACACACAGCTGCCATTGTAGCTAATTGCTTTGTGTTCTGATTGA 850
 QY 26 TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysIleAspProLysAla 45
 DB 851 TACATGGTATTTTCGAGGAGCAACCAAGCAAGCATGTGTTCAAAAGAAATCCAAAGGCT 910
 QY 46 ProIleTyrGlyLysProLysValValGlyGlyLysLeuLeuAlaSerGlyTyrTrp 65
 DB 911 CCTATCTGGGTAAAGCTCCAAAGTCATTTGGTGAAGTACTTGTCTTCTGTTATTGG 970
 QY 66 GlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeu 85
 DB 971 GGTATTGCTAGACACTGTAATTACCTAGGGGATTTGATGCTTCTCTCTTACGTTA 1030
 QY 86 ProCysGlyValSerValValProTyrPheTyrPheTyrProTyrLeuLeuLeuLeu 105
 DB 1031 CCATGTGGGATAAGTTCACCAATTCACATCTTATCCAAATTTATCTTCTTATTCTGTTA 1090
 QY 106 ValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTyrPala 125
 DB 1091 ATCTGGAGAGAGAGAGGATGAAGCTCGTTGCGCGAGAGATATAGAGAGATATGGGCC 1150
 QY 126 GluTyrCysLysLeuValProTyrPheTyrPheTyrValTyr 140
 DB 1151 GAGTATCGTAAACTTGTTCCTCAAGGAGATATTTGCTTACGTTAT 1195

RESULT 4

AAF30677

ID AAF30677 standard; cDNA; 1364 BP.

XX AAF30677;

XX 11-JUN-2001 (first entry)

XX Soybean sterol delta-14 reductase clone ssm.pk0031.d12.fis.

XX Soybean; sterol delta-14 reductase; transgenic plant; herbicide;
 KW fungicide; ss.

XX Glycine max.

XX Key Location/Qualifiers
 FT CDS 64..1173
 FT /*tag= a
 FT /partial

XX WO200123539-A2.

XX 05-APR-2001.

XX 27-SEP-2000; 2000WO-US026442.

XX 30-SEP-1999; 99US-0156820P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Famodu OO, Kinney AJ;

XX WPI; 2001-266146/27.

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DR P-PSDB; AAB20381.
XX
XX Novel gene encoding sterol delta-14 reductase useful for transgenic plant
PT production with altered sterol delta-14 reductase.
XX
XX Claim 7; Page 39; 45pp; English.
XX
CC The present sequence is that of the full insert sequence of clone
CC sm.p0031.d12, which includes a full-length coding region for soybean
CC sterol delta-14 reductase (see AAB20381). The clone was isolated from a
CC soybean shoot meristem cDNA library, following homology searches. The
CC predicted protein shows amino acid sequence homology to Arabidopsis
CC thaliana and Ascorbolus immerus sterol delta-14 reductases. The invention
CC relates to isolated polynucleotides encoding sterol delta-14 reductases
CC and to transgenic plants comprising such polynucleotides. It also relates
CC to the construction of a chimeric gene encoding all or a portion of the
CC sterol delta-14 reductase, in sense or antisense orientation, where
CC expression of the chimeric gene results in production of altered levels
CC of the enzyme in a transformed host cell. The availability of plant
CC sterol delta-14 reductase genes will provide a means of altering sterol
CC production and/or composition of plants, to identify compounds that may
CC be useful as novel herbicides and fungicides, and to identify mutants of
CC these genes that are resistant to these herbicides and will enable the
CC production of herbicide-resistant crops
XX
SQ Sequence 1364 BP; 346 A; 277 C; 296 G; 445 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.32e-68 Length: 1364
Score: 621.00 Matches: 111
Percent Similarity: 91.85% Conservative: 13
Best Local Similarity: 82.22% Mismatches: 11
Query Match: 82.25% Indels: 0
DB: 4 Gaps: 0

US-10-069-427-6 (1-140) x AAF30677 (1-1364)
Qy 6 AsnLysValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIleGly 25
Db 766 AACAGTGTGGAGTTACACAGCAGTCCCATTTAGTAAATTTGTTTCTCTGATTGGA 825
Qy 26 TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspProLysAla 45
Db 826 TACATGTATTTTCAGGAGCAACAAAGCATGTGTTCAAAAGATCCAAAGGCT 885
Qy 46 ProIleTrpGlyLysProLysValValGlyLysLeuAlaSerGlyTyrTrp 65
Db 886 CCTATCTGGGTAAAGCCTCCAAAGTCATTGGTGGAAAGTACTTGTCTTGTATTGG 945
Qy 66 GlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeu 95
Db 946 GGTATTGCTAGACTGTAATACCAATTCACATCTTCTATTCATTCGTTA 1005
Qy 86 ProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuLeuLeu 105
Db 1006 CCAATGTGGATAAGTTCACCAATTCACATCTTCTATTCATTCGTTA 1065
Qy 106 ValLeuArgGluArgArgAspGluAlaArgCysSerGlnLysTyrArgGluLeuTrpAla 125
Db 1066 ATCTGGAGAGAGAAACCGATGAAGCTCGTTGGCCGAGAGATATAGAGATATCGGCC 1125
Qy 126 GluTyrCysLysLeuValProTyrArgIleLeuProTyrValTyr 140
Db 1126 GAGTATCGTAACATTGTTCCATGGAGATATTCCTTACGTTAT 1170

RESULT 5
AAC37623
ID AAC37623 standard; DNA; 1380 BP.
XX
XX AAC37623;
XX
XX 17-OCT-2000 (first entry)
DT
XX

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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 18063.
XX
XX Hybridisation assay; Genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
OS
XX
XX EP1033405-A2.
PN
XX 06-SEP-2000.
PD
XX 25-FEB-2000; 2000EP-00301439.
PF
XX
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-0123548P.
XX 23-MAR-1999; 99US-0125788P.
XX 25-MAR-1999; 99US-0126264P.
XX 29-MAR-1999; 99US-0126785P.
XX 01-APR-1999; 99US-0127462P.
XX 06-APR-1999; 99US-0128234P.
XX 08-APR-1999; 99US-0128714P.
XX 16-APR-1999; 99US-0129845P.
XX 19-APR-1999; 99US-0130077P.
XX 21-APR-1999; 99US-0130449P.
XX 23-APR-1999; 99US-0130510P.
XX 28-APR-1999; 99US-0130891P.
XX 30-APR-1999; 99US-0131449P.
XX 30-APR-1999; 99US-0132048P.
XX 04-APR-1999; 99US-0132407P.
XX 04-MAY-1999; 99US-0132484P.
XX 05-MAY-1999; 99US-0132485P.
XX 06-MAY-1999; 99US-0132486P.
XX 07-MAY-1999; 99US-0132487P.
XX 07-MAY-1999; 99US-0132863P.
XX 11-MAY-1999; 99US-0134256P.
XX 14-MAY-1999; 99US-0134218P.
XX 14-MAY-1999; 99US-0134219P.
XX 14-MAY-1999; 99US-0134221P.
XX 14-MAY-1999; 99US-0134370P.
XX 18-MAY-1999; 99US-0134768P.
XX 19-MAY-1999; 99US-0134941P.
XX 20-MAY-1999; 99US-0135124P.
XX 21-MAY-1999; 99US-0135353P.
XX 24-MAY-1999; 99US-0135629P.
XX 25-MAY-1999; 99US-0136021P.
XX 27-MAY-1999; 99US-0136392P.
XX 28-MAY-1999; 99US-0136782P.
XX 01-JUN-1999; 99US-0137232P.
XX 03-JUN-1999; 99US-0137528P.
XX 07-JUN-1999; 99US-0137502P.
XX 07-JUN-1999; 99US-0137724P.
XX 08-JUN-1999; 99US-0138094P.
XX 10-JUN-1999; 99US-0138540P.
XX 10-JUN-1999; 99US-0138847P.
XX 14-JUN-1999; 99US-0139119P.
XX 16-JUN-1999; 99US-0139452P.
XX 16-JUN-1999; 99US-0139453P.
XX 17-JUN-1999; 99US-0139492P.
XX 18-JUN-1999; 99US-0139454P.
XX 18-JUN-1999; 99US-0139455P.
XX 18-JUN-1999; 99US-0139456P.
XX 18-JUN-1999; 99US-0139457P.
XX 18-JUN-1999; 99US-0139458P.
XX 18-JUN-1999; 99US-0139459P.
XX 18-JUN-1999; 99US-0139460P.
XX 18-JUN-1999; 99US-0139461P.
XX 18-JUN-1999; 99US-0139462P.
XX 18-JUN-1999; 99US-0139463P.
XX 18-JUN-1999; 99US-0139750P.
XX 18-JUN-1999; 99US-0139763P.
XX 21-JUN-1999; 99US-0139817P.

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Db 998 GGAATTCGACGACCTGTAATACCTTGGGACCTGATGCTGCTGCTCCCTCAGTTTG 1057
Qy 86 ProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuLeuLeu 105
Db 1058 CCATGTGGAATAAGTCTCCGGTTCCTCATATTTCTACCCGATATACCTTCTGATACTATTG 1117
Qy 106 ValLeuArgGluArgArgGluAlaArgCysSerClnIlystYrArgGluIleTTPAla 125
Db 1118 ATATGGGAGAACGACGACGAGGTTCGATGTCGAGAGAGTACAGGAGATATGGCA 1177
Qy 126 GluTyrCysIlystLeuValProTTPArgIleLeuProTyrValTyr 140
Db 1178 GAGTATCTTAGACTTGCTCCCTCGAGATACCTTCCTTATGTTAT 1222

RESULT 6
AAC45795
ID AAC45795 standard; DNA, 1110 BP.
AC AAC45795;
XX
XX
DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 47790.
KW Hybridisation assay; Genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EF1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 03-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139452P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144522P.
PR 20-JUL-1999; 99US-0144523P.
PR 20-JUL-1999; 99US-0144524P.
PR 21-JUL-1999; 99US-0144525P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145313P.
PR 27-JUL-1999; 99US-0145318P.
PR 28-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 03-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.


```

XX PS Claim 7; Fig 14; 71pp; English.
XX CC cDNA clone D13 includes a coding region for a novel C-14 sterol reductase
XX CC (see AAW41576) of Arabidopsis thaliana. An Arabidopsis mutant, ell (extra
XX CC long life), that displayed a life span that was at least 3 times greater
XX CC than wild-type plants, was isolated. The ell mutant was isolated by T-DNA
XX CC tagging, and used to screen cDNA and genomic libraries from a wild-type
XX CC plant to identify clone D13 and a 6588 bp genomic clone (see AAV04238). A
XX CC pure plant C-14 sterol reductase (C14SR) is claimed, as are purified DNA
XX CC encoding C14SR, a vector, a method of producing recombinant C14SR using
XX CC transformed plant cells, a transgenic plant that expresses C14SR DNA and
XX CC a seed or cell from such a plant, and methods for detecting and isolating
XX CC a C14SR gene, and for reducing the level of C14SR in a transgenic plant
XX CC using an antisense construct. The genetic manipulation of plant sterol
XX CC composition is useful for improving food quality and oil stability, and
XX CC for regulating the formation of compounds having anti-nutritional, and
XX CC properties. Reduced production of C14SR can increase the life-span of
XX CC plants and produce plants having reduced and more compact proportions.
XX CC Overproduction is useful for enhancing the production of medically or
XX CC agriculturally useful steroid compounds. C14SR polypeptides are also
XX CC useful for the development of enzyme inhibitors of the sterol
XX CC biosynthetic pathway
XX SQ Sequence 1429 BP; 369 A; 269 C; 305 G; 481 T; 0 U; 5 Other;

Alignment Scores:
Pred. No.: 1.17e-66 Length: 1429
Score: 609.00 Matches: 107
Percent Similarity: 90.37% Conservative: 15
Best Local Similarity: 79.26% Mismatches: 13
Query Match: 80.66% Indels: 0
DB: 2 Gaps: 0

US-10-069-427-6 (1-140) x AAV04237 (1-1429)
Qy 6 AsnLysValGluLeuSerLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIleGly 25
Db 786 AACAAAGTAGAAGTAACTGCTGCGATTGTAGTCAATGCGCTTCTTGTATAGG 845
Qy 26 TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspProLysAla 45
Db 846 TACATGGTTTTCGAGGAGCTAACAAACAAACATATCTTTAAGAAAGAACCCAAACA 905
Qy 46 ProIleTrpGlyLysProLysValValGlyGlyLysLeuAlaSerGlyTyrTrp 65
Db 906 CCAATATGGGCAAGCCCTCAGTGGTAGTGGTGAAGTTACTGGTTTCAGGCTATTGG 965
Qy 66 GlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeu 85
Db 966 GGAATTGCAAGGCACGTGTAATTACCTTGGCGACTTGATGCTGCTCTCCTTCAGTTTG 1025
Qy 86 ProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuLeuLeu 105
Db 1026 CCATGTGGAATAAGTTCTCCGGTTCATATTTCTACCCGATATACCTTCTGATCTATTG 1085
Qy 106 ValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTrpAla 125
Db 1086 ATATGGAGAGACGAGAGAGAGAGTTCGATGTGCGAGAGAGTACAGGAGATATGGCA 1145
Qy 126 GluTyrCysLysLeuValProTrpArgIleLeuProTyrValTyr 140
Db 1146 GAGTATCTTAGACTTGTCCCTCGAGAACTTCTCTATGTTTAT 1190

RESULT 8
AAV04238
ID AAV04238 standard; cDNA; 6588 BP.
XX AC AAV04238;
XX XX
XX DT 22-JUN-1998 (first entry)
XX XX
XX DE Arabidopsis C-14 sterol reductase genomic DNA.

XX KW C-14 sterol reductase; ELL gene; transgenic plant; steroid;
XX KH crop improvement; ds.
XX OS Arabidopsis thaliana.
XX FH Key Location/Qualifiers
FT transposon 3055..3175 /tag= a
FT exon /note= "T-DNA insert"
FT 3356..3486 /tag= b
FT CDS /number= 1
FT 3439..6178 /tag= ac
FT intron /note= "contains 13 introns"
FT 3487..3584 /tag= c
FT exon /number= 1
FT 3585..3703 /tag= d
FT intron /number= 2
FT 3704..3794 /tag= e
FT exon /number= 2
FT 3795..3865 /tag= f
FT intron /number= 3
FT 3866..3977 /tag= g
FT exon /number= 3
FT 3978..5023 /tag= p
FT exon /number= 8
FT 3978..4032 /tag= h
FT intron /number= 4
FT 4033..4144 /tag= i
FT exon /number= 4
FT 4145..4236 /tag= j
FT intron /number= 5
FT 4237..4576 /tag= k
FT exon /number= 5
FT 4577..4624 /tag= l
FT intron /number= 6
FT 4625..4771 /tag= m
FT exon /number= 7
FT 4772..4891 /tag= n
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FT 4892..4977 /tag= o
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FT 5194..5340 /tag= s
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FT 5341..5420 /tag= t
FT exon /number= 10
FT 5421..5496 /tag= u
FT intron /number= 10

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 FT exon 6223..6588
 FT /*tag= ab
 FT /number= 14
 FT intron 6244..6262
 FT /*tag= aa
 FT /number= 13

PN W09748793-A1.

XX 24-DEC-1997.

XX 20-JUN-1997; 97WO-US010644.

XX 21-JUN-1996; 96US-0022086P.

XX (GEHO) GEN HOSPITAL CORP.

XX Jang J, Sheen J;

XX WPI; 1998-063134/06.

XX P-PSDB; AAW41576.

XX New isolated plant C-14 sterol reductase gene - used to develop products
 PT for the genetic manipulation of a plant sterol biosynthetic pathway to
 PT improve plant characteristics.

XX Claim 28; Fig 15; 71pp; English.

XX This genomic DNA includes coding exons for a novel C-14 sterol reductase
 CC (see AAW41576) of Arabidopsis thaliana. An Arabidopsis mutant, ell (extra
 CC long life), that displayed a life span that was at least 3 times greater
 CC than wild-type plants, was identified. The ell mutant was isolated by T-
 CC DNA tagging, and used to screen genomic and cDNA libraries from a wild-
 CC type plant to identify the 6588 bp genomic clone and cDNA clone D13 (see
 CC AAW04237). A pure plant C-14 sterol reductase (C14SR) is claimed, as are
 CC purified DNA encoding C14SR, a vector, a method of producing recombinant
 CC C14SR using transformed plant cells, a transgenic plant that expresses
 CC C14SR DNA and a seed or cell from such a transgenic plant, and methods
 CC for detecting and isolating a C14SR gene, and for reducing the level of
 CC C14SR in a transgenic plant using an antisense construct. The genetic
 CC manipulation of plant sterol composition is useful for improving food
 CC quality and oil stability, and for regulating the formation of compounds
 CC having anti-nutritional properties. Reduced production of C14SR can
 CC increase the life-span of plants and produce plants having reduced and
 CC more compact proportions. Overproduction is useful for enhancing the
 CC production of medically or agriculturally useful steroid. C14SR
 CC polypeptides are also useful for the development of enzyme inhibitors of
 CC the sterol biosynthetic pathway

XX Sequence 6588 BP; 1857 A; 1255 C; 1227 G; 2169 T; 0 U; 80 Other;

XX Alignment Scores:

Pred. No.:	1.95e-51	Length:	6588
Score:	496.00	Matches:	107
Percent Similarity:	44.49%	Conservative:	14
Best Local Similarity:	39.34%	Mismatches:	137
Query Match:	65.70%	Indels:	3
DB:	2	Gaps:	3

US-10-069-427-6 (1-140) x AAV04238 (1-6588)

QY 6 AsnLysValGluLeuSerGlyLeuAlaAsnLeuCysIlePheLeuile-G1 25

Db 5362 AACAAAGTAGAACTAACAAATTCCTGCGATTGTAGTCAATTGCCTTGCTTCTTATAGGG 5421

QY 25 Y-----

Db 5422 TAAAGTCTGAGACATGGGGTTATTTTCCATTCTTACATATCTACACTAAGAAACCCACTA 5481

QY 26 -----TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLy 40

Db 5482 TTTCTCTTTGGCAGGTACATGGTTTTTCGAGGAGCTAACAAACAAAACATAATCTTTAA 5541

QY 40 slyAspProLysAlaProIleTyrGlyLeuProLysValValGlyGlyLeuLe 60

Db 5542 GAAGAAACCAAAACACCAATATGGGCAAGCTCCAGTGGTAGTTGGTGAAGATTACT 5601

QY 60 uAlaSerGlyTyrTrp-----

Db 5602 GGTTCAGGCTATTGGTATGTTATATTATCTCTCTTTGTTCTTTGTTCTTGGTTCGCCA 5661

QY 65 -----

Db 5662 TCTCTGTGTTGATTGTTTCATCATGCTCGGAATAAAGAGTTGAAAGTTCCGCAATGACAC 5721

QY 66 -----GlyIleAlaArgHisCysAs 72

Db 5722 ATTTCCGATAACTTAGGTGCTGTTTGTATATATGACAGGGGAATTCGAAGGCACTGTAA 5781

QY 72 nTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeuProCysGlyVal----- 89

Db 5782 TTACCTTGGGCACTTGATGCTTGCTCTGCTCTGCTTTCAGTTTGCCATGCGAATAGGTACTC 5841

QY 89 -----

Db 5842 CTNCTGCTTGAGTTCACTTACAGCTACCAGCAATCATGTAGAAACTATATACCAATATCNAA 5901

QY 89 -----

Db 5902 ACGTTCGAAGTTGATTGGCTGACTTAAAGATATTGATCTCTAACCATCATTGAAAAAGT 5961

QY 89 -----

Db 5962 CTAAAGCTTTCAAGTTTCATTTCCCAAGCTGTTTTTATGATATTTCGTCTNGTGTATTCT 6021

QY 90 -SerSerValValProTyrPheTyrProThrTyrLeuLeuLeuLeuValLeuArgG1 109

Db 6022 CAGTTCTCGGGTTCATATTTCTACCCGATATACCTGCTGATCTATTGATATGGAGAGA 6081

QY 109 uArgArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTrpAlaGluTyrCysLy 129

Db 6082 ACGAAGAGACGAAGTTCCGATGTCAGAGAGTACNAGGAGATATGCGCAGAGATCTTAG 6141

QY 129 sleuValProTrpArgIleLeuProTyrValTyr 140

Db 6142 ACTTGTCCTCGGAAATACCTTCCTTATGTTTAT 6175

QY 6142 ACTTGTCCTCGGAAATACCTTCCTTATGTTTAT 6175

QY 6142 ACTTGTCCTCGGAAATACCTTCCTTATGTTTAT 6175

QY 6142 ACTTGTCCTCGGAAATACCTTCCTTATGTTTAT 6175

QY 6142 ACTTGTCCTCGGAAATACCTTCCTTATGTTTAT 6175

QY 6142 ACTTGTCCTCGGAAATACCTTCCTTATGTTTAT 6175

QY 6142 ACTTGTCCTCGGAAATACCTTCCTTATGTTTAT 6175

QY 6142 ACTTGTCCTCGGAAATACCTTCCTTATGTTTAT 6175

QY 6142 ACTTGTCCTCGGAAATACCTTCCTTATGTTTAT 6175

QY 6142 ACTTGTCCTCGGAAATACCTTCCTTATGTTTAT 6175

QY 6142 ACTTGTCCTCGGAAATACCTTCCTTATGTTTAT 6175

QY 6142 ACTTGTCCTCGGAAATACCTTCCTTATGTTTAT 6175

QY 6142 ACTTGTCCTCGGAAATACCTTCCTTATGTTTAT 6175

QY 6142 ACTTGTCCTCGGAAATACCTTCCTTATGTTTAT 6175

QY 6142 ACTTGTCCTCGGAAATACCTTCCTTATGTTTAT 6175

```
XX PN WO200210436-A2.
XX XX
XX PD 07-FEB-2002.
XX XX
XX PF 27-JUL-2001; 2001WO-US023642.
XX XX
XX PR 28-JUL-2000; 2000US-0222093P.
XX XX
XX PA (BGM) BRIGHAM & WOMENS HOSPITAL INC.
XX PA (BAK/) BAAK J.
XX XX
XX PI Baak J, Mutter GL;
XX XX
XX XX WPI; 2002-180084/23.
XX DR P-PSDB; AAUB4347.
XX XX
XX PT Diagnosing breast cancer comprises determining expression of nucleic acid
XX PT molecules or expression products that are differentially expressed in
XX PT normal and malignant tissue.
XX XX
XX PS Claim 1; Page 94-96; 219pp; English.
XX XX
XX CC The present invention relates to a method for diagnosing breast cancer in
XX CC a subject suspected of having endometrial cancer. The method comprises
XX CC determining the expression of a set of human genes or expression products
XX CC in an endometrial sample suspected of being cancerous. The human genes of
XX CC the invention are differentially expressed in breast tumours
XX CC characterised as high or low MAI (mitotic activity index). These sets of
XX CC genes can be used to discriminate between high and low MAI breast
XX CC tumours. The invention also provides DNA and protein microarrays for
XX CC analysing the expression of the human genes and their protein products.
XX CC The methods and arrays are useful for the diagnosis and prognosis of
XX CC endometrial cancer, selecting and monitoring treatment regimes, and
XX CC identification of compounds useful for the treatment of endometrial
XX CC cancer. ABK35531-ABK35581 represent the human genes of the invention that
XX CC are differentially expressed in breast cancer tissue
XX XX
XX SQ Sequence 3714 BP; 1046 A; 644 C; 759 G; 1265 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3 78e-34 Length: 3714
Score: 356.50 Matches: 67
Percent Similarity: 64.75% Conservative: 23
Best Local Similarity: 48.20% Mismatches: 33
Query Match: 47.22% Indels: 16
DB: 6 Gaps: 2

US-10-069-427-6 (1-140) x ABK35567 (1-3714)
Qy 12 LeuLeuSerGlyLeuAlaAsnLeuOys-llePheLeuIleGlyLeuValPheArgGl 31
Db 1524 TTGCCAATGGCTTCTTAATTATTCTTCTGAACCTTGTGGTATGTAATCTTCGAGG 1583
Qy 31 YAlaAsnLysGlnLysHisValPheLysLysAspProLysAlaProIleTyrGlyLysPr 51
Db 1584 TGAATATCTCAGAAAATCCATTCGGAAAATCC-----AGTGA 1625
Qy 51 oProLysValVal-----GlyGlyLysLeuLeuAlaLase 62
Db 1626 TCCAAAGCTTGACATTTAAACCATTCTATCTCAAGTGGAAAAATCTTCTAGTTTC 1685
Qy 62 rGlyTyrTyrGlyLleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLase 82
Db 1686 TGGATGGGGGTTTGTTCGCCACCCCAATTAATCTTGGTGATCTCATCATGGCCTTGGC 1745
Qy 82 rPheSerLeuProCysGlyValSerSerValProTyrPheTyrProThrTyrLeuLeu 102
Db 1746 GTGGTCCCTCCCATGGTGTGTTTAAACCACATCTGCTTATTTCTACATAATTTATTCAC 1805
Qy 102 uIleLeuValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGl 122
Db 1806 CATGTTGCTGTCCACCGAAGACTCGTACCGAGTACCACCTGTAAAGAGAAATACGGCGT 1865
```

Qy 122 uIleTyrAlaGluTyrCysLysLeuValProTyrPheArgIleLeuProTyrValTyr 140
Db 1866 GCCTTGGGAAAAGTACTGTCTAGCGTGTGCCCTACGTATATTTCCATACATCTAC 1920

RESULT 10
ABK3864
ID ABK3864 standard; cDNA; 3714 BP.
XX
AC ABK3864;
XX
DT 14-AUG-2002 (first entry)
XX
DE Human cDNA differentially expressed in granulocytic cells #435.
XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
OS Homo sapiens.
XX
XX WO200228999-A2.
XX
XX 11-APR-2002.
XX
XX 03-OCT-2001; 2001WO-US030821.
XX
XX 03-OCT-2000; 2000US-0237189P.
XX
XX (GENE-) GENE LOGIC INC.
XX
XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
XX WPI; 2002-435328/46.
XX
XX Detecting granulocyte activation by detecting differential expression of
XX genes associated with granulocyte activation, which serves as diagnostic
XX markers that is useful for monitoring disease states and drug toxicity.
XX
XX Claim 1; SEQ ID NO 435; 114pp; English.
XX
XX The invention relates to detecting (M1) granulocyte (GC) activation
XX (GCA) by detecting the level of expression of gene(s) (Gs) identified by
XX DNA chip analysis as given in the specification, and comparing the
XX expression level to an expression level in an unactivated GC, where
XX differential expression of Gs is indicative of GCA. Also included are
XX modulating (M2) GA by contacting GC with an agent that alters the
XX expression of at least one gene in Gs; (2) screening (M3) for an agent
XX capable of modulating GCA or an inflammation (especially chronic) in a
XX tissue, an allergic response in a subject, exposure of a subject to a
XX pathogen or sterile inflammatory disease using the gene expression
XX profile; (3) detecting (M4) an inflammation (especially chronic) in a
XX tissue, an allergic response in a subject, exposure of a subject to a
XX pathogen or sterile inflammatory disease, by detecting the level of
XX expression in a sample of the tissue of gene(s) from Gs, where the level
XX of expression of the gene is indicative of inflammation; (4) treating
XX (M5) an inflammation (especially chronic) or in a tissue, an allergic
XX response in a subject, exposure of a subject to a pathogen or sterile
XX inflammatory disease, by contacting a tissue having inflammation with an
XX agent that modulates the expression of gene(s) from Gs in the tissue. M1
XX is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful
XX for screening an agent capable of modulating GCA preferably in an
XX inflammation in a tissue; M4 is useful for detecting an inflammation
XX (especially chronic) in a tissue, an allergic response in a subject,
XX exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
XX psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
XX cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
XX respiratory distress syndrome, inflammatory bowel disease, Crohn's

CC disease, ulcerative colitis, periodontal disease; also bacterial
 CC infection, viral infection, parasitic infection, protozoal infection,
 CC fungal infection and M5 is useful for treating one of the above
 CC conditions. The present sequence represents a gene differentially
 CC expressed in granulocytes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 3714 BP; 1046 A; 644 C; 759 G; 1265 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3,78e-34 Length: 3714
 Score: 356.50 Matches: 67
 Percent Similarity: 64.75% Conservative: 23
 Best Local Similarity: 48.20% Mismatches: 33
 Query Match: 47.22% Indels: 16
 DB: 6 Gaps: 2

US-10-069-427-6 (1-140) x ABK83864 (1-3714)

QY 12 LeuLeuSerGlyLeuAlaAanLeuCys-11ePheLeuIleGlyTyrLeuValPheArgG1 31
 DB 1524 TTGGCCAAATGGCTTCTCTAATATTGTTCTGAACATTTGGTTATGTAATCTCCGAGG 1583
 QY 31 YAlaAsnLysGlnLysHisValPheLysLysAspProLysAlaProIleTrrpGlyLysPr 51
 DB 1584 TGCAATTCCTCAGAAAATGCAATCCGAAAAATCCC-----AGTGA 1625
 QY 51 oProLysValVal-----GlyGlyLysLeuLeuAlaSe 62
 DB 1626 TCCAAAGCTTGCACATTTAAAAACCAATTCATCTCAAGTGGAAAAATCTTAGTTTC 1685
 QY 62 rGlyTyrTrpGlyLeuAlaAargHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSe 82
 DB 1686 TGGATGTGGGGCTTTGTTGCCACCCCAATTAATCTGGTGATCTCATCATGCGCTTGGC 1745
 QY 82 rPheSerLeuProCysGlyValSerSerValProTyrPheTyrProThrTyrLeuLe 102
 DB 1746 GTGGTCCCTCCCATGTGGTTTAAACCAATCTGCCTTATTCTACATATTTATTTCAC 1805
 QY 102 uIleLeuLeuValLeuGluArgAspGluAlaArgCysSerGlnLysTyrArgG1 122
 DB 1806 CATGTGCTTGTCCACCGAAGCTCGTGACGAGTACCACCTGTAAAGAAATACGCGCT 1865
 QY 122 uIleTrrpAlaGluTyrCysLysLeuValProTrrpArgIleLeuProTrrpValTyr 140
 DB 1866 GCCTTGGGAAAAGTACTGTGACGCTGTGCGCTACCGTATATTTCCATACATCTAC 1920

RESULT 11

ADB56005/c
 ID ADB56005 standard; DNA; 476 BP.

XX AC ADB56005;

XX AC ADB56005;

XX AC ADB56005;

XX AC ADB56005;

XX AC ADB56005;

XX AC ADB56005;

XX AC ADB56005;

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XX AC ADB56005;

XX AC ADB56005;

XX AC ADB56005;

XX AC ADB56005;

XX AC ADB56005;

XX AC ADB56005;

PR 30-DEC-2002; 2002US-0436643P.

XX (GENE-) GENE LOGIC INC.

XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;

XX WPI; 2003-689530/65.

XX Predicting a toxic effect of a compound, useful in identifying toxicity
 markers in liver tissues or cells for drug screening and toxicity assays,
 PT comprises preparing gene expression profile of tissue or cells exposed to
 PT the compound.

XX Claim 1; SEQ ID NO 1031; 1156pp; English.

XX The present invention relates to a method for predicting a toxic effect
 of a compound. The method comprises preparing a gene expression profile
 of a tissue or cell sample exposed to the compound, and comparing the
 gene expression profile to a database comprising SEQ ID 1-4925, where
 CC differential expression of the gene indicates at least one toxic effect.
 CC The method is useful for predicting at least one toxic effect of a
 CC compound, predicting hepatotoxicity or the progression of a toxic effect
 of a compound, identifying an agent that modulates the onset or
 CC progression of a toxic response, predicting the cellular pathways that a
 CC compound modulates in a cell, and identifying an agent that modulates at
 CC least one activity of a protein. The method and compositions of the
 CC present invention using a database of genes having liver toxin-induced
 CC differential expression, are useful in identifying toxicity markers in
 CC liver tissues or cells for drug screening and toxicity assays. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 476 BP; 110 A; 119 C; 124 G; 123 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 5,58e-31 Length: 476
 Score: 321.50 Matches: 59
 Percent Similarity: 70.2% Conservative: 19
 Best Local Similarity: 53.15% Mismatches: 30
 Query Match: 42.58% Indels: 3
 DB: 9 Gaps: 1

US-10-069-427-6 (1-140) x ADB56005 (1-476)

QY 33 AsnLysGlnLysHisValPheLysLysAspProLysAlaProIleTrrpGlyLysProPro 52

DB 476 AATCCCGAGAAAATACATTCAGAAAAGATCCTTCTGACCCAGTGTGGCTGTGAG 417

QY 53 LysValVal-----GlyGlyLysLeuLeuAlaSerGlyTyrTrrpGlyLeuAlaArg 69

DB 416 ACCATCTTACTGCCAGCGGAGGAGCTGTGTGTCTGGTGTGGGTATGTTTGA 357

QY 70 HisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeuProCysGlyVal 89

DB 356 CACCCCAACTACTTGGGAGACCTCATGCTGTGGTGTGGTGTGGTGTGGTGTGG 297

QY 90 SerSerValValProTyrPheTyrProThrTyrLeuLeuIleLeuValLeuArgGlu 109

DB 296 TCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 237

QY 110 ArgArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTrrpAlaGluTrrpCysLys 129

DB 236 GCCCGAGATGACGACGAGTGCCTGCGAAAGTATGCGCGTGCCTGCAGGAATACTGCAAG 177

QY 130 LeuValProTrrpArgIleLeuProTrrpValTyr 140

DB 176 CGCGTGCCTTACCGAATCATACCGTATGTCTAC 144

RESULT 12

AAF26559

ID AAF26559 standard; DNA; 1896 BP.

XX

AAF26559;
 27-MAR-2001 (first entry)
 DNA encoding human secreted protein #13.
 Secreted protein; gene therapy; vaccine; cancer; leukemia;
 autoimmune disease; allergy; inflammation; graft rejection;
 hyperproliferation; cardiovascular; infection; ss.
 Homo sapiens.
 WO200076531-A1.
 21-DEC-2000.
 01-JUN-2000; 2000WO-US015137.
 11-JUN-1999; 99US-0138625P.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Ruben SM, Komatsoulis GA;
 WPI; 2001-071148/08.
 Nucleic acids encoding 47 human secreted polypeptides, useful for
 preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease
 and diabetic retinopathy.
 Claim 1; Page 449-454; 525pp; English.
 The present invention relates to 26 secreted human proteins. The proteins
 may be used in the prevention, diagnosis and treatment of diseases
 associated with inappropriate polypeptide expression. For example, they
 may be used in gene therapy or in vaccines. Typical of diseases which are
 potentially treatable are cancers (including leukemia), autoimmune
 diseases, allergies, inflammation, graft rejection, hyperproliferation,
 cardiovascular diseases (particularly critical limb ischemia and coronary
 disease) and any involving abnormal angiogenesis, neurodegeneration
 and/or infectious diseases
 Sequence 1896 BP; 351 A; 582 C; 516 G; 444 T; 0 U; 3 Other;
 Alignment Scores:
 Pred. No.: 6.99e-30 Length: 1896
 Score: 319.50 Matches: 63
 Percent Similarity: 60.96% Conservative: 26
 Best Local Similarity: 43.15% Mismatches: 44
 Query Match: 42.32% Indels: 13
 DB: 4 Gaps: 2
 US-10-069-427-6 (1-140) x AAF26559 (1-1896)
 QY 8 ValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuLeuGlyTyrLeu 27
 DB 471 GTGAGCTGTCCACCCCGACGCGGTGGGCTCTGCTGCTGGGCTGTGGCTACTAC 530
 QY 28 ValPheArgGlyAlaAsnLysGlnLysHisValPheLysLys---AspProLysAlaPro 46
 DB 531 ATCTTCGGGTGGTCCAAACACCAAGAGGACCTGTTCCTCCCGCAGCGATGGGCGTCC 590
 QY 47 IleTrrpGlyLysProLysValVal----- 55
 DB 591 ATCTGGGCGAGGAAGCCCAAGGTCTATCGAGTCTCTACATCCGCCGACGGGACAGG 650
 QY 56 ---GlyGlyLysLeuLeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeu 74
 DB 651 CACACAGCAAGCTGTGTGTGGGCTTCTGGGCGGTGGCCGCACTTCAACTACGTC 710
 QY 75 GlyAspLeuLeuAlaLeuSerPheSerLeuProCysGlyValSerValValPro 94
 DB 711 GGCGACCTGTATGGGACGCTGGCCCTACTGCTGGCTGTGGCGTGGCCACCTGCTGCC 770

QY 95 TyrPheTyrProThrTyrLeuLeuIleLeuLeuValLeuArgGluArgAspGluAla 114
 DB 771 TACTTCTACATCATCTACATCGCATCTGCTGACCCACCGCTCCCTCCGGGACGAC 830
 QY 115 ArgCysSerGlnLysTyrArgGluIleTrpAlaGluTyrCysLysLeuValProTrrArg 134
 DB 831 CGTGTGGCCAGCAAGTAGTCGGCGGGACTGGGAGCGCTACACCGCGCGAGTTCCTTACCGC 890
 QY 135 IleLeuProTyrValTyr 140
 DB 891 CTGCTGCCTGGAATCTTC 908
 RESULT 13
 AAX90448
 ID AAX90448 standard; cDNA; 2481 BP.
 XX
 AC AAX90448;
 XX
 DT 29-SEP-1999 (first entry)
 XX
 DE Human secreted protein clone pj323_2 nucleotide sequence.
 XX
 KW Human; secreted protein; nutrition; cytokine; cell proliferation;
 differentiation; immune stimulating; vaccine; suppression; gene therapy;
 haematopoiesis regulation; tissue growth; activin; inhibin; cadherin;
 chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory;
 tumour invasion suppressor; tumour inhibition; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 78..1505
 FT /*tag= a
 FT /product= "secreted protein"
 XX
 PN WO9937674-A1.
 XX
 PD 29-JUL-1999.
 XX
 PF 21-JAN-1999; 99WO-US001404.
 XX
 PR 22-JAN-1998; 98US-0072134P.
 PR 20-JAN-1999; 99US-00235609.
 XX
 XX (GENY) GENETICS INST INC.
 PA
 PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Merberg D;
 PI Treacy M, Agostino MJ, Steininger RJ, Wong GG, Clark HF, Fecht K;
 XX
 DR WPI; 1999-458682/38.
 DR P-PSDB; AAY29333.
 XX
 PT New polynucleotides encoding secreted human proteins derived from, e.g.
 PT fetal brain potentially used as immunostimulators.
 XX
 PS Claim 33; Page 126; 139pp; English.
 CC
 CC The present sequence encodes a human secreted protein. Human secreted
 CC protein polynucleotides and proteins are predicted to have biological
 CC activities which would make them suitable for treating, preventing or
 CC ameliorating medical conditions in humans and animals, although no
 CC supporting data is given. Suggested activities include nutritional
 CC activity, cytokine and cell proliferation/differentiation activity,
 CC immune stimulating (e.g. as vaccines) or suppressing activity,
 CC haematopoiesis regulating activity, tissue growth activity,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, cadherin/tumour invasion suppressor activity, and tumour
 CC inhibition activity. The polynucleotides are also stated to be useful for
 CC gene therapy
 XX
 SQ Sequence 2481 BP; 471 A; 764 C; 655 G; 589 T; 0 U; 2 Other;

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Alignment Scores:
Pred. No.: 1.02e-29 Length: 2481
Score: 319.50 Matches: 63
Percent Similarity: 60.96% Conservative: 26
Best Local Similarity: 43.15% Mismatches: 44
Query Match: 42.32% Indels: 13
DB: 2 Gaps: 2

US-10-069-427-6 (1-140) x AAX90448 (1-2481)
Qy 8 ValGluLeuSerLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIleGlyTyrLeu 27
Db 1065 GTGAGCTGTCCACCGCGCGGCTGCTGCTGGGCTGTGGCTACTAC 1124
Qy 28 ValPheArgGlyAlaAsnLysGlnLysHisValPheLysLys---AspProLysAlaPro 46
Db 1125 ATCTCCGGGTGCCCAACCCAGAGGACCTGTTCGGCGCGGATGGCGCTGCCTC 1184
Qy 47 IleTrpGlyLysProLysValVal----- 55
Db 1185 ATCTGGGCGAGGAGCCAGGTCATCGAGTGCTCTACATCCGCGCGGCGAGAGG 1244
Qy 56 ---GlyGlyLysLeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeu 74
Db 1245 CACCACAGCAAGCTGCTGTGGGCTCTGGGCGCTGGCGCGGACCTCAACTACGTC 1304
Qy 75 GlyAspLeuLeuAlaLeuSerPheSerLeuProCysGlyValSerSerValValPro 94
Db 1305 GGCACCTGATGGCGAGCCTGGCTACTGCTGCTGGCTGGCGGTGCCACCTGCTGCC 1364
Qy 95 TyrPheTyrProThrTyrLeuLeuIleLeuValLeuArgGluArgAspGluAla 114
Db 1365 TACTTCTACATCATCTAGCCATCTGCTGACCCACCGCTGCTCCCGGACGAGCAC 1424
Qy 115 ArgCysSerGlnLysTyrArgGluIleTrpAlaGluTyrCysLysLeuValProTyrArg 134
Db 1425 CGCTGCCCGACAGTAGCGCGGAGTGGAGCGCTACACCGCGGAGTGCCTTACCGC 1484
Qy 135 IleLeuProTyrValTyr 140
Db 1485 CTGCTGCTGAATCTTC 1502

RESULT 14
AAS59277
ID AAS59277 standard; cDNA; 2481 BP.
XX AC AAS59277;
XX DT 16-JAN-2002 (first entry)
XX DE Human cDNA encoding a secreted protein pJ323_2.
XX KW Human; secreted protein; ss; antiinflammatory; immunosuppressive;
KW nootropic; neuroprotective; antiarthritic; antimicrobial; vulnery;
KW cytostatic; antidiabetic; virucide; antifertility; anticonvulsant;
KW vasotropic; antiparkinsonian; immunostimulant; dermatological;
KW antirheumatic; antitumor; antitumor; osteopathic; tranquilizer;
KW cerebrotective; cytokine; cell proliferation; cell differentiation;
KW immune deficiency; severe combined immunodeficiency; SCID; tumor;
KW autoimmune disorder; multiple sclerosis; rheumatoid arthritis;
KW graft-versus-host disease; myeloid deficiency; wound healing; ulcer;
KW periodontal disease; osteoporosis; osteoarthritis; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; infection; cardiac disease;
KW stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
KW food supplement.
XX OS Homo sapiens.
XX PN WO200175068-A2.
XX XX
XX PD 11-OCT-2001.
XX XX
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Tue Jun 15 08:54:16 2004

Qy 115 ArgCysSerGlnLysTyrArgGluIleTrpAlaGluTyrCysLysLeuValProTrpArg 134
Db 1425 CGCTGGCCAGCAAGTACGGCCGGGACTGGGAGCGCTACACCGCGCGAGTGCCTTACCGC 1484
Qy 135 IleLeuProTyrValTyr 140
Db 1485 CTGCTGCTGGAACTTC 1502

Search completed: June 14, 2004, 10:02:16
Job time : 236.291 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2004, 14:36:55 ; Search time 24.6483 Seconds
(without alignments)
772.871 Million cell updates/sec

Title: US-10-069-427-8
Perfect score: 1965
Sequence: 1 MMESHVDLGLLQALTPSN.....REINAEYKLVPRILPVY 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/2/aaa/5B-COMB.pep:*
3: /cgn2_6/prodata/2/aaa/6A-COMB.pep:*
4: /cgn2_6/prodata/2/aaa/6B-COMB.pep:*
5: /cgn2_6/prodata/2/aaa/PCUS-COMB.pep:*
6: /cgn2_6/prodata/2/aaa/backfills.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1561.5	79.5	368	4	US-08-879-337-1
2	657	33.4	145	4	US-09-342-653-4
3	641	32.6	418	4	US-09-342-653-7
4	630	32.1	615	4	US-08-879-337-9
5	575.5	29.3	424	4	US-08-879-337-5
6	568	28.9	637	4	US-08-879-337-8
7	549.5	28.0	438	4	US-08-879-337-4
8	549	27.9	419	1	US-08-439-131A-3
9	549	27.9	419	1	US-08-440-674-2
10	547.5	27.9	438	1	US-08-439-131A-2
11	547.5	27.9	438	1	US-08-440-674-5
12	443.5	22.6	432	4	US-09-443-041A-20
13	441.5	22.5	450	4	US-09-443-041A-22
14	434	22.1	430	4	US-09-443-041A-18
15	415.5	21.1	430	1	US-08-601-435-2
16	415.5	21.1	430	2	US-08-931-047-2
17	415.5	21.1	430	2	US-08-783-202-2
18	415.5	21.1	430	4	US-09-443-041A-31
19	401	20.4	81	4	US-09-342-653-6
20	354.5	18.0	453	1	US-08-439-131A-5
21	354.5	18.0	453	1	US-08-440-674-4
22	354.5	18.0	453	1	US-08-879-337-6
23	354	18.0	473	1	US-08-439-131A-4
24	354	18.0	473	1	US-08-440-674-3
25	354	18.0	473	4	US-08-879-337-7
26	308	15.7	68	4	US-09-342-653-2
27	121	6.2	591	4	US-09-134-000C-5399

28	109	5.5	620	4	US-09-540-236-3109	Sequence 3109, Ap
29	107.5	5.5	538	4	US-09-252-991A-23060	Sequence 23060, A
30	107.5	5.5	650	3	US-08-800-291B-4	Sequence 4, Appli
31	106.5	5.4	649	3	US-08-800-291B-5	Sequence 5, Appli
32	106.5	5.4	649	3	US-08-800-291B-6	Sequence 6, Appli
33	104	5.3	336	4	US-09-252-991A-20404	Sequence 20404, A
34	104	5.3	336	3	US-09-068-195-24	Sequence 24, Appl
35	104	5.3	514	4	US-09-252-991A-20338	Sequence 20338, A
36	103.5	5.3	648	3	US-08-800-291B-8	Sequence 8, Appli
37	102	5.2	466	4	US-09-489-039A-14325	Sequence 14325, A
38	101.5	5.2	236	3	US-09-095-758-12	Sequence 12, Appl
39	101.5	5.2	236	3	US-09-422-968-12	Sequence 12, Appl
40	101.5	5.2	236	4	US-09-708-015A-12	Sequence 7299, Ap
41	100.5	5.1	532	4	US-09-107-532A-7299	Sequence 7515, Ap
42	100.5	5.1	567	4	US-09-543-681A-4765	Sequence 4765, Ap
43	99.5	5.1	358	4	US-09-328-352-6961	Sequence 6961, Ap
44	96.5	4.9	414	4	US-09-252-991A-32657	Sequence 32657, A
45	96	4.9	597	4		

ALIGNMENTS

RESULT 1
US-08-879-337-1
; Sequence 1, Application US/08879337B
; Patent No. 6639130
; GENERAL INFORMATION:
; APPLICANT: Jang, Jyan-Chyun
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
; FILE REFERENCE: 00786/338001
; CURRENT APPLICATION NUMBER: US/08/879,337B
; CURRENT FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/022,086
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-08-879-337-1

Query Match	79.5%	Score	1561.5	DB	4	Length	368
Best Local Similarity	79.3%	Pred. No.	6.2e-153				
Matches	292	Conservative	28	Mismatches	39	Indels	9
Gaps	2						
QY	6	VDLGLLQALTPSKNSVPLNGFFTYLAVAGSILPGKLVPGVALLDGTPLHYCCNGLISL	65				
Db	5	MDLGVLL-----PSLQSVVLVVFYFVYLAAGEILPGKVRGVLSDGSQLEKRCNGLLAL	60				
QY	66	LLVALLGIGAKMGFVSPFATSDRGLLELLSTTFAPSPFLVTLILHPSGCKSOSKSSLKPH	125				
Db	61	ILLVAILGICAKLGIVSPVAVDRGLELLSATFICVLVTLVTLVYTCRSSNKGSSLKPH	120				
QY	126	LSGNLHNDHWFGIQLNPFMGIDLK-----AGVMGMLLINLSILMKSTQDGTLSQSMILY	180				
Db	121	VSGNLVHDWFGIQLNPFMGIDLKFFVFRAGMGMMLLINLSILAKSVQDSLSQSMILY	180				
QY	181	QLFCALYILDYFVHEEYNTSTWDIIAERLGMPLVFGDLVWIPFSPFISQGMWLLNNSVBLT	240				
Db	181	QIFCALYILDYFVHEEYNTSTWDIIAERLGMPLVFGDLVWIPFSPFISQGMWLLNNSVBLT	240				
QY	241	PAAIYVNCVFLIGYVWFRGANKQKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPK	300				
Db	241	VPVAVVNCVFLIGYVWFRGANKQKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPK	300				
QY	301	NYLGLMLALGFSPLPCGISSPFPYPIYLLIILWERTDEARCAEKYRIWAEYKLV	360				
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QY	361	PWRILPVY 368					

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Db      361 PWRLPYV 368
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RESULT 2
US-09-342-653-4
; Sequence 4, Application US/09342653
; Patent No. 6306632
; GENERAL INFORMATION:
; APPLICANT: Caboon, Rebecca E.
; TITLE OF INVENTION: Chromatin Associated Proteins
; FILE REFERENCE: BB-1118
; CURRENT APPLICATION NUMBER: US/09/342,653
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/092,841
; EARLIER FILING DATE: July 14, 1998
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-342-653-4

Query Match      33.4%; Score 657; DB 4; Length 145;
Best Local Similarity 80.1%; Pred. No. 4.4e-60;
Matches 113; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Qy      229 GWMMLNSVELTPAAIVANCFVLIGYVFRGANKOKHVFKKNKRAPIMGKPKVIGGKL 288
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Db      5 GWMLLRNKVELSLAAVAVNCFFIVIGYVFRGANKOKHIFKKNPKALINGKPKLVGGKL 64
|||||
Qy      289 LASGYGIAHCHNYLGDMLALSFSLPCGSSPIPYPIYLLILILWRERTDEARCAEK 348
|||||
Db      65 LVSGYGIACHNYLGDMLALSFSLPCGTSVPIPYPTYLIFILLWRERDEARCSEK 124
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Qy      349 YREIMAEYKLVFWRLPYV 369
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Db      125 YKEIWVEYCKLVFWRLPYV 145
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RESULT 3
US-09-342-653-7
; Sequence 7, Application US/09342653
; Patent No. 6306632
; GENERAL INFORMATION:
; APPLICANT: Caboon, Rebecca E.
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Chromatin Associated Proteins
; FILE REFERENCE: BB-1118
; CURRENT APPLICATION NUMBER: US/09/342,653
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/092,841
; EARLIER FILING DATE: July 14, 1998
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-342-653-7

Query Match      32.6%; Score 641; DB 4; Length 418;
Best Local Similarity 40.6%; Pred. No. 8.5e-58;
Matches 152; Conservative 69; Mismatches 131; Indels 22; Gaps 13;

Qy      12 LQALTPSNVSVLLVGFYTLAVAGS--ILPG-KLVPGVALLDGTRLHYCCNGLLSLLL 68
|||||
Db      51 LPLGVLSFRAILL-LWALGLQALYLLPARKVAEGQELKDSRURYPINGFOALVLT 109
|||||
Qy      69 VALLGIGAKMGVSPSTAISDRGLELSTTFAPSFVLTLILHFSGCKSQ-SKGSSLKPK-HL 126
|||||

Db      110 ALLVGLGMSAG-LPLGALPEMLLPLAFVATILATAFISLFLYM---KAQVAPVSALAPGQN 165
|||||
Qy      127 SGNLIHDMWFQIQLNPOFMGID-----LKAGMMGWLILNLSILMKSIQ-DGTILSQSMIL 179
|||||
Db      166 SGNFIYDFLGLREINPRICFFDFKYFCELRPLGLIGWVLINLALLMKAEALRGSPSLAWWL 225
|||||
Qy      180 YQLFCALYILDYFVHEEYMTSTWDIIAERLGFMLVFGDLVMIIPFSFIQGWMLLMSVEL 239
|||||
Db      226 VNGFQLLYVGDALWHEERAVLTMDITHDGFGEMLAFCDMAWVFTYSLQAQFLLHHPQL 285
|||||
Qy      240 -TPRAIVANCFVFLIGYVFRGANKOKHVFKKNKAP-IMGKP--PKVIQKLLASGYWG 295
|||||
Db      286 GLPMASVI-CLINAIGYIIFRGANSQKNTFRKNPSDPRVAGLETISTATGRKLLVSGWNG 344
|||||
Qy      296 IARHCNYLGDMLALSFSLPCGSSPIPYPIYLLILILWRERTDEARCAEKYREIWA 355
|||||
Db      345 MVRHPNYLGDMLALSLPCGVSHLLPYLYLYFFALLVHREARDEQCLOKYGAWQE 404
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Qy      356 YRKLVPWRILPYV 369
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Db      405 YCREVPYRIMPYIY 418
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RESULT 4
US-08-879-337-9
; Sequence 9, Application US/08879337B
; Patent No. 6639130
; GENERAL INFORMATION:
; APPLICANT: Jang, Jyan-Chyun
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
; FILE REFERENCE: 00786/338001
; CURRENT APPLICATION NUMBER: US/08/879,337B
; CURRENT FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/022,086
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-879-337-9

Query Match      32.1%; Score 630; DB 4; Length 615;
Best Local Similarity 38.5%; Pred. No. 2e-56;
Matches 145; Conservative 65; Mismatches 127; Indels 40; Gaps 11;

Qy      8 LGFLQALTPSNVSVLLVGFYTLAVAGSILP-KGLVPGVALLDGTRLHYCCNGLLSLL 66
|||||
Db      264 LWFLIQVL-----FY-----LLPIGKVGESTPLIDGRRLKYRLNGFYPI 303
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Qy      67 LLVALLGIGAKMGVSPSTAISDRGLELSTTFAPSFVLTLILHFSGCKSQSGSSLKPHL 126
|||||
Db      304 LTSAVIGTSLFOG-VEFYHYVSHFLQFALAAVFCVLSVLYMRSLKAPR--NDLSPAS 360
|||||
Qy      127 SGNLIHDMWFQIQLNPOFMGIDLK-----AGMMGWLILNLSILM--KSIQDGTL-SQSM 177
|||||
Db      361 SGNVYDFPIGRLNPRIGTDLKYFCELRPLGLIGWVLINLALLMKAEALRGSPSLAM 420
|||||
Qy      178 ILYQLFCALYILDYFVHEEYMTSTWDIIAERLGFMLVFGDLVMIIPFSFIQGWMLL--N 235
|||||
Db      421 ILVNSFQLLYVVDALWNEBALLTTMDIHDGFGFMLAFGDLVWVFPFYFQAFYLVSHPN 480
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Qy      236 SVBLTPAAIVANCFVFLIGYVFRGANKOKHVFKKNKAPIMGKPKPV--IGGKLLASG 292
|||||
Db      481 EYSWPNASII--IVLKCGYVIFRGANSQKNAFRKNPSDPKLAHLKTHITSSGKLLVSG 538
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Qy      293 YGCIARHCNYLGDMLALSFSLPCGSSPIPYPIYLLILILWRERTDEARCAEKYREI 352
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|||||
Qy      353 WAERYKLVWRILPYV 369
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Db 173 KONGREKILAGGN-SNIIYDFIGRELNPRGLDIFKMFSLRPGMLWLLNLS 231
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Db 232 CLHHYLTGKINDALVNFLOQGYIFDGLNBEGLVTWMDITTDGFGFLAFGLSLV 291
Qy 222 PFSIGOWLLMNSVELTAAIVANCVFLLGYMVRGANKOKHVKKNPKAPIWGKPP 281
Db 292 PFTISQARLYSPVSELGWKVVGGIILMFLGFHIFHSANKOKSEFROCKLENLSIOT 351
Qy 282 KVIGGKLLASGYGIAHRCNYLGLDMLALSFLPCGSISSPIFYFYIYLLIILWERTD 341
Db 352 K-RGTLKLLCGWAKSQHINFGDWLISLWCLATWFOPLTYYSLYPATLLHRRQD 410
Qy 342 EARCAEKYREIWAERYKLVPWILPVY 369
Db 411 EHKRLKYGENWEEYERKVPKIIPVY 438

RESULT 8
US-08-439-131A-3
; Sequence 3, Application US/08439131A
; Patent No. 5512472
; GENERAL INFORMATION:
; APPLICANT: Lai, Margaret H. K.
; APPLICANT: Bard, Martin
; APPLICANT: Kirsch, Donald R.
; TITLE OF INVENTION: A DNA Sequence Encoding Sterol Delta
; Patent No. 5512472
; TITLE OF INVENTION: Reductase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,131A
FILING DATE: 11-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,347
FILING DATE: 16-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Alan M.
REGISTRATION NUMBER: 30,637
REFERENCE/DOCKET NUMBER: 854-012 (32,141)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3244
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
AUTHORS: Worman, H. J.
AUTHORS: Evans, C. D.
AUTHORS: Biobel, G.
TITLE: The Lamin B Receptor of the Nuclear Envelope
JOURNAL: J. Cell Biol.
VOLUME: 111

; PAGES: 1535-1542
; DATE: 1990
; RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 190 TO 608
; US-08-439-131A-3

Query Match 27.9%; Score 549; DB 1; Length 419;
Best Local Similarity 36.1%; Pred. No. 2.7e-48;
Matches 136; Conservative 69; Mismatches 132; Indels 40; Gaps 12;

Qy 12 LQALTPSMNS---VPLLVGFYTLAVAGSILP-GKLVPGVALLDGRFLHYCCNGLSL 66
Db 50 LPALESIMWETKVFVGLLWFFQALFY---LLPTGKVVVEGLPLSNPKPKQYRINGFYAFL 106
Qy 67 LLVA---LLGIGAKYGFVSPSTAISDRGLELLSTTFASFLVTLILHFSCKSQSKSSL 122
Db 107 LTAATQTLFYQFELHY---LYDHFVQFAVSAAFSMALSYLYIRSLKAPEE--DL 159
Qy 123 KP-HLSGNLIHDMWFGIQLNPFQFMGIDLK-----AGMGMGLINLSIL---MKSIOGT 172
Db 160 APGNSGYLVNPFTHGELNPRIGSFDLYKFCFLRPGIGVWVNLAMLLAEMKHNQSM 219
Qy 173 LSQSMILYQLFCALYILDYFVHEEYNTWTDIIABRLGFMVFGDLVMIWIPFSIQGWL 232
Db 220 PLSMILVNSFQLLYVVDALWNEEAVLTMDITDHDGFGFLAFGLVWVFPVYSLOFYI 279
Qy 233 LMNSVELT---PAAIVANCVFLLGYMVRGANKOKHVKKNPKAP---IWGKPKVIG 285
Db 280 VGHPIAISWPVAAAITILNC-----IGYIFRSANSQKNFRNFPADPKLSYLVKVIPTATG 335
Qy 286 GKLLASGYGIAHRCNYLGLDMLALSFLPCGSISSPIFYFYIYLLIILWERTDEARC 345
Db 336 KGLLVTCWVGFRHPNYLGDIIIMALWSLPCGFGHILPYFYIYFICLLVHREARDEHHC 395
Qy 346 AEKYREIWAERYKLVPW 362
Db 396 KKKYGLAWERYCQRPVY 412

RESULT 9
US-08-440-674-2
; Sequence 2, Application US/08440674
; Patent No. 5525496
; GENERAL INFORMATION:
; APPLICANT: Margaret H. Lai
; TITLE OF INVENTION: A DNA Sequence Encoding Sterol
; Patent No. 5525496
; TITLE OF INVENTION: Reductase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07470
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,674
FILING DATE: May 15, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,347
FILING DATE: August 16, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Alan M. Gordon
REGISTRATION NUMBER: 30637
REFERENCE/DOCKET NUMBER: 854-P0012 Div (32,141)
TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-831-3244
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
FEATURE:
NAME/KEY: chicken
NAME/KEY: nuclear lamin B receptor
PUBLICATION INFORMATION:
AUTHORS: H.J. Worman, C.D. Evans, and G.
AUTHORS: Bichel
TITLE: (excerpt): The Lamin B Receptor of the
TITLE: Nuclear Envelope Inner Membrane
JOURNAL: Journal of Cell Biology
VOLUME: 111
PAGES: 1535-1542
PAGES: Sequence set out in Figure 5, page 1539
Patent No. 5525496
DATE: 1990
RELEVANT RESIDUES IN SEQ ID NO: 190 to 608
US-08-440-674-2

Query Match 27.9%; Score 549; DB 1; Length 419;
Best Local Similarity 36.1%; Pred. No. 2.7e-48;
Matches 136; Conservative 69; Mismatches 132; Indels 40; Gaps 12;
QY 12 LQALTPSWNS---VPLVGVFFYLAVAGSIPL-GKLVPGVALLDGTTRHYCCNGLLSL 66
DB 50 LPALSLWETKVFVGLFWFFQALFY---LLPIGVKVEGLPLSNPRKQYRNGFYAPL 106
QY 67 LLVA---LLGIGAKGVFSPTAISDRGLELLSTTFASFVLTLIHFSGCKSQSGSSL 122
DB 107 LTAALQTLVYFQFELHY-----LYDHVQVPAVSAAFSMALSIYIRSLKAPEE--DL 159
QY 123 KP-HLSGNLHDMWFGIQLNPQPMGIDLK-----AGMGWLLINLSIL---MKSIGDOT 172
DB 160 APGNGSYLVNFTGHELNPRIGSFDLYFCFLRPLGLIGWVIVNLAEMKHINQSM 219
QY 173 LSOSMILYQLCALYILDYFVHEEYMTSTWDIATRLGMLVFGDLVWIPFSGSIQGWML 232
DB 220 PSLSMILVNSQLLYVVVDALWNEEAVLTITDTHDGFGLMFAFGDLVWVFFVYSLQAFYI 279
QY 233 LMSNVLT---PAAIVANCVFVLIGYVFRGANKQKHVFNKPKAP----IWGKPKVIG 285
DB 280 VGHPIAISWFAAAITLNC---IGYIIFRSANSQKNFRNFPADPKLSYLKVIPTATG 335
QY 286 GKLLASGYGIARHCNVLGDLMLALSPLSGISPIPGYPIYLLILLIWRERTDEAR 345
DB 336 KGLLVTCGWGVRHPNVLGDIIMALWSLPCGFGNHLPLVPYVIYFICLLVHREARDEHHC 395
QY 346 AEKREIWAERYKLVVPV 362
DB 396 KKKIGLAWERYQRPVY 412

RESULT 10
US-08-439-131A-2
Sequence 2, Application US/08439131A.
Patent No. 5512472
GENERAL INFORMATION:
APPLICANT: Lai, Margaret H. K.
APPLICANT: Bard, Martin
APPLICANT: Kirsch, Donald R.
TITLE OF INVENTION: A DNA Sequence Encoding Sterol Delta
Patent No. 5512472
TITLE OF INVENTION: Reductase
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:

ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07470
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,131A
FILING DATE: 11-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,347
FILING DATE: 16-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Alan M.
REGISTRATION NUMBER: 30,637
REFERENCE/DOCKET NUMBER: 854-012 (32,141)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3244
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-439-131A-2

Query Match 27.9%; Score 547.5; DB 1; Length 438;
Best Local Similarity 34.3%; Pred. No. 4.1e-48;
Matches 133; Conservative 76; Mismatches 136; Indels 43; Gaps 11;
QY 19 WNSV-PL--LVG-----FFYLAVAGSIPLGKLVPGVALLDGTTRHYCCNGLLSL 65
DB 57 WNGIKPLRYILGNRELWTVYCLWYGILAVLDVILPGRVMKGVQLRDSGLSKYKINGIAMS 116
QY 66 LLLVALLGIGAK-----MGFVSPTAISDRGLELLSTTFASFVLTV-----LIL 108
DB 117 TTLVLVLAIRWKLTDGQLPELOYLYENHVS---LCIISILFSF-FLATYCVASFIPLIF 172
QY 109 HFGCKSQSGSKSLPHLSGNLIHDWFGIQLNPQPMGIDLK-----AGMGWLLINLS 162
DB 173 KXNGKREKIALGNGN-SGNIYDWFIGRELNPLGFLDIKMFSELRLPGMLLWLLINLS 231
QY 163 ILMKS-IDQGTLSOSMILYQLFALYILDYFVHEEYMTSTWDIATRLGMLVFGDLVWI 221
DB 232 CLUHHYLTGKINDALVNVNFSQGFYIFDGVNBEGLVMTMDITTDGFGFMLAFDGLSLV 291
QY 222 PFSFSIQGWLLMNSVELTPAAIVANCVFVLIGYVFRGANKQKHVFNKPKAPITWGKPP 281
DB 292 PFTYSLQARYLSVSPVELGWVKVGCILAIMFLGHIHFSAANKQSEFFQGLKLENLSIOT 351
QY 282 KVIIGKLLASGYGIARHCNVLGDLMLALSPLSGISPIPGYPIYLLILLIWRERTD 341
DB 352 K-RGTKLLCDGWAKSQHINYFGDWLISLWCLATWFOTPLTYYSYSLYFATILLHQORD 410
QY 342 EARCAREIWAERYKLVVPV 369
DB 411 EHKRLKYGENWEEYERKVPYKIIIPVY 438

RESULT 11
US-08-440-674-5
Sequence 5, Application US/08440674
Patent No. 5525496
GENERAL INFORMATION:
APPLICANT: Margaret H. Lai
TITLE OF INVENTION: A DNA Sequence Encoding Sterol

Patent No. 5525496
; TITLE OF INVENTION: 14
; TITLE OF INVENTION: Reductase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07470
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processor
; CURRENT APPLICATION DATA: US/08/440,674
; FILING DATE: May 15, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/107,347
; FILING DATE: August 16, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Alan M. Gordon
; REGISTRATION NUMBER: 30637
; REFERENCE/DOCKET NUMBER: 854-P0012 Div (32,141)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; DESCRIPTION: polypeptide
; IMMEDIATE SOURCE: Saccharomyces cerevisiae
; IMMEDIATE SOURCE: clone
; FEATURE:
; OTHER INFORMATION: translated polypeptide of
; OTHER INFORMATION: sterol 14
; OTHER INFORMATION: reductase gene
US-08-440-674-5

Query Match 27.9%; Score 547.5; DB 1; Length 438;
Best Local Similarity 34.3%; Pred. No. 4.1e-48;
Matches 133; Conservative 76; Mismatches 136; Indels 43; Gaps 11;

QY 19 WNSV-PL--LVG-----FFYLAVAGSILPGKLVPGVALLDGTRLHYCNGLLSL 65
Db 57 WNGIKPLRYLGNRELVTWYICLWYIGILAVLDVILPGRVKGVLQDRDGSKLYKINGIAMS 116

QY 66 LLLVALLGIGAK-----MGFVSPATISDRGLELLSTTFAPSLVT-----LIL 108
Db 117 TTLVLVLAIRKLTQQLPELOYIYENHVS---LCIIISILFSP-FLATYCVASFIPLIF 172

QY 109 HPSGCKSQSGKSLKPHLSGNLIHDWFGIOLNPFQMGIDLK-----AGMGWLLINLS 162
Db 173 KKGNGKREKILALGNGN-SGNIYDWFIGRELNPLGLDIDKMFSELPGMLLMLINLS 231

QY 163 ILKMS-IDGTLTQSMLYQLFCALYILDYFVHEEYMTSTWDIIAERLGFMLVFGDLVWI 221
Db 232 CLHHYLYKTKINDALVNLVNSQGYIFIDGVNLNEGVLTMDDITDQGFGLMFGDLJSLV 291

QY 222 PPSFIQGWNLMSVETTPAAIVANCFVFLIGYVFRGANKQKHVFKKPNKAPINGKPP 281
Db 292 PFTYSLOARYLSVSVELGVKAVGVIGILAIMELGFHIFHSANKQKSEFRQGLKLEKSIQT 351

QY 282 KVIQGLKLSAGVWGIFARHCNVLGDLMLALSLSLPCGISSPPIYPYPIYLLILLWRD 341

Db 352 K-RGTYLLCDGWNAKSHQINYFGDWLISLSWCLATWTFQTPUTYYYSLYFATLLHROORD 410
QY 342 EARCAEKYREIWAERYKLVPWRILPYVY 369
Db 411 EHKRLKYGNEWEVERKVPYKIIPYVY 438

RESULT 12
US-09-443-041A-20
; Sequence 20, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Glycine max
US-09-443-041A-20

Query Match 22.6%; Score 443.5; DB 4; Length 432;
Best Local Similarity 30.4%; Pred. No. 2.2e-37;
Matches 119; Conservative 75; Mismatches 153; Indels 45; Gaps 12;

QY 12 LQAL-----TPSNVSPLLVGFFTYLAVAGSILPGKLVPGVALLDGTRLHYCNGL---- 62
Db 52 LOGLLHIWPTPTPTACKIIAIVAAFAALQLLPGKTVGPISPTGHRPVPYKANGLOAYF 111

QY 63 LSLILLVALLGIGAKMGFVSPTAISDRGLELLSTTFAPSLVTLLIHFSGCKSQSGSSL 122
Db 112 VTLITYPALWW---FGIFNPTIVYHHLGEISALIFGSLFCVFLYIKGHLAPSTDS- 166

QY 123 KPHLSGNLIHDWFGIOLNPFQ-MGIDLK-----GMMGWLLINLSILMKSIQD-GTUS 174
Db 167 --GSSGNLIIDFYGMELYPRIKGFEDIKVTNCRFGMMSWAVLALTYCIKQVEENGKVA 224

QY 175 QSMILYQLFCALYILDYFVHEEYMTSTWDIIAERLGFMLVFGDLVWIPFSFIQGWLLM 234
Db 225 DMLVNTALMLVTVTFWWEAGYWTMDIADHAGFYICWGLVWVPSVYTSFGMYLVN 284

QY 235 N-----SVELTPAAIVANCFVFLIGYVFRGANKQKHVFKK-NPKAPIWGKPKVI----- 284
Db 285 HPVNLGIGKLSILVAGILCIYNY-----DCDQRQEPRTNGKGTVMGKAPSKIEATYT 340

QY 285 --GGK-----LLASGYWGIFARHCNVLGDLMLALSLSLPCGISSPPIYPYPIYLLILLWR 337
Db 341 TTSGTKRSELLTSGWGLSRHFHYVPEILAAFFVTVPALFEHFLPYFYVIELTILFDR 400

QY 338 ERTDEARCAEKYREIWAERYKLVPWRILPYVY 369
Db 401 AKRDDRCSKYKYWKLYCDKVPYRIIPGIY 432

RESULT 13
US-09-443-041A-22
; Sequence 22, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes

FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 22
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-09-443-041A-22

Query Match 22.5%; Score 441.5; DB 4; Length 450;
Best Local Similarity 29.7%; Pred. No. 3.8e-37;
Matches 117; Conservative 79; Mismatches 151; Indels 47; Gaps 14;

QY 11 LQALTPSNNVPLLV-----GFTYLAAGSILPGKLVPGVALLDGTTRLHYCCNGLLS 64
DB 69 VLEGLKAIW-PMTLVANWKLIFGGLFEAVLQQLLPCKRFEFGPISPAGNVVYKANGLOA 127
QY 65 -LLLLVALLGIGAKMGFVSPTAISDRGLELLSTTFAPSLVTLILHFSG---CKSQSKGS 120
DB 128 YAVTLITYLGLW-WFGIFNPAIVDHLGEIYSALVFGSFVFCIFLYIKGHVFPSSSDGS 186
QY 121 SLKPHLSGNLIHDWTFGIQNPQF-MGIDLK-----GMMGMLLINLSILMKSQ-DGT 172
DB 187 -----SGNVIIDFYWGMELYPRIKGFIDKVTNCRFGMMSWAVLAVTYCIKQVEMGR 240
QY 173 LSQSMILYQFCALYITLDYFVHEEYMTSTWIIAERLGMFLVFGDLVWIPFSFSIQGWL 232
DB 241 VADSLVNTALMIYITKFFWESSGYCTMDIAHADRAGFYICWGLVWVPSIYTSFGMYL 300
QY 233 LMSNVELTP-----AAIVANCFVFLIGYVFRGANKQKHVFK-NPKAPTWGK-PKVI 285
DB 301 VNHPLNLGQALSIILLAGMLCIYINY-----DCDRQROEFRRTNGKCSWGRKAPSKI 356
QY 286 -----GKLLASGYWGIAHCHNYGLDMLALSFCGSISSPIPYFYPIYLLILIMR 340
DB 357 YQTKGETKSLTSGWGLSRHFVPEILSAFWTPALFDHFLPYFYVIFLTLILF 416
QY 336 WRERTDEARCAEYREINWBYRKLVPWRILPVY 369
DB 417 DRAKRDDRCSKYGYKWKYCNKVPVRIPGIY 450

RESULT 14
US-09-443-041A-18
; Sequence 18, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-443-041A-18

Query Match 22.1%; Score 434; DB 4; Length 430;
Best Local Similarity 29.0%; Pred. No. 2.1e-36;
Matches 113; Conservative 77; Mismatches 157; Indels 42; Gaps 12;

QY 12 LQALTPSNNVPLLV-----GFTYLAAGSILPGKLVPGVALLDGTTRLHYCCNGLLS 65
DB 53 LKAIWPMPTWAANK---IIFGGLFEALQQLLPCKRFEFGVSPSGNVVYKANGLOAYA 109
QY 66 LLLVALLGIGAKMGFVSPTAISDRGLELLSTTFAPSLVTLILHFSGCKSQSKSLKPH 125
DB 110 VTLITYLSLW-WFGIFNPAIVDHLGEIYSALVFGSFVFCIFLYIKGHVFPSSSDS---G 165
QY 126 LSGNLIHDWTFGIQNPQF-MGIDLK-----GMMGMLLINLSILMKSQ-DGTLSQSM 177
DB 166 SSGNVIIDFYWGMELYPRIKGFIDKVTNCRFGMMSWAVLAVTYCIKQVEMGRVADSM 225
QY 178 ILYQFPCALYITLDYFVHEEYMTSTWIIAERLGMFLVFGDLVWIPFSFSIQGWL 237
DB 226 LVNTALMIYVTRKFFWESSGYCTMDIAHADRAGFYICWGLVWVPSIYTSFGMYLVNHPV 285
QY 238 ELTP-----AAIVANCFVFLIGYVFRGANKQKHVFK-NPKAPTWGKPKVI----- 284
DB 286 NLGQALSIILLAGMLCIYINY-----DCDRQROEFRRTNGKCSWGRKAPSKI 341
QY 285 -----GKLLASGYWGIAHCHNYGLDMLALSFCGSISSPIPYFYPIYLLILIMR 340
DB 342 GETKSSLLTSGWGLSRHFVPEILSAFWTPALFDHFLPYFYVIFLTLILFDRKR 401
QY 341 DEARCAEYREINWBYRKLVPWRILPVY 369
DB 402 DDCRCSKYGYKWKYCNKVPVRIPGIY 430

RESULT 15
US-08-601-435-2
; Sequence 2, Application US/08601435
; Patent No. 5759801
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA sequence coding for a protein
; TITLE OF INVENTION: Of A, thaliana having a delta-5,7 sterol, delta-7
; TITLE OF INVENTION: reductase activity, delta-7-Red protein, production
; TITLE OF INVENTION: process, strains of transformed yeasts, uses.
; NUMBER OF SEQUENCES: 31
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/601,435
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9501723
; FILING DATE: 15-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9506517
; FILING DATE: 01-JUN-1995
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-601-435-2

Query Match 21.1%; Score 415.5; DB 1; Length 430;
Best Local Similarity 29.7%; Pred. No. 1.7e-34;
Matches 116; Conservative 78; Mismatches 153; Indels 43; Gaps 15;

QY 12 LQALTPSNNVPLLV-----GFTYLAAGSILPGKLVPGVALLDGTTRLHYCCNGLLS 65
DB 52 VOGLININWR-PTLAWKLIIFCYGFAEAILQLLPCKRVEGPISPAGNVVYKANGLAAY 110
QY 66 LLLVAL-LGIGAKMGFVSPTAISDRGLELLSTTFAPSLVTLILHFSGCKSQSKSLK 124

FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 22
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-09-443-041A-22

Query Match 22.5%; Score 441.5; DB 4; Length 450;
Best Local Similarity 29.7%; Pred. No. 3.8e-37;
Matches 117; Conservative 79; Mismatches 151; Indels 47; Gaps 14;

QY 11 LQALTPSNNVPLLV-----GFTYLAAGSILPGKLVPGVALLDGTTRLHYCCNGLLS 64
DB 69 VLEGLKAIW-PMTLVANWKLIFGGLFEAVLQQLLPCKRFEFGPISPAGNVVYKANGLOA 127
QY 65 -LLLLVALLGIGAKMGFVSPTAISDRGLELLSTTFAPSLVTLILHFSG---CKSQSKGS 120
DB 128 YAVTLITYLGLW-WFGIFNPAIVDHLGEIYSALVFGSFVFCIFLYIKGHVFPSSSDGS 186
QY 121 SLKPHLSGNLIHDWTFGIQNPQF-MGIDLK-----GMMGMLLINLSILMKSQ-DGT 172
DB 187 -----SGNVIIDFYWGMELYPRIKGFIDKVTNCRFGMMSWAVLAVTYCIKQVEMGR 240
QY 173 LSQSMILYQFCALYITLDYFVHEEYMTSTWIIAERLGMFLVFGDLVWIPFSFSIQGWL 232
DB 241 VADSLVNTALMIYITKFFWESSGYCTMDIAHADRAGFYICWGLVWVPSIYTSFGMYL 300
QY 233 LMSNVELTP-----AAIVANCFVFLIGYVFRGANKQKHVFK-NPKAPTWGK-PKVI 285
DB 301 VNHPLNLGQALSIILLAGMLCIYINY-----DCDRQROEFRRTNGKCSWGRKAPSKI 356
QY 286 -----GKLLASGYWGIAHCHNYGLDMLALSFCGSISSPIPYFYPIYLLILIMR 340
DB 357 YQTKGETKSLTSGWGLSRHFVPEILSAFWTPALFDHFLPYFYVIFLTLILF 416
QY 336 WRERTDEARCAEYREINWBYRKLVPWRILPVY 369
DB 417 DRAKRDDRCSKYGYKWKYCNKVPVRIPGIY 450

RESULT 14
US-09-443-041A-18
; Sequence 18, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-443-041A-18

Query Match 22.1%; Score 434; DB 4; Length 430;
Best Local Similarity 29.0%; Pred. No. 2.1e-36;
Matches 113; Conservative 77; Mismatches 157; Indels 42; Gaps 12;

QY 12 LQALTPSNNVPLLV-----GFTYLAAGSILPGKLVPGVALLDGTTRLHYCCNGLLS 65
DB 53 LKAIWPMPTWAANK---IIFGGLFEALQQLLPCKRFEFGVSPSGNVVYKANGLOAYA 109
QY 66 LLLVALLGIGAKMGFVSPTAISDRGLELLSTTFAPSLVTLILHFSGCKSQSKSLKPH 125
DB 110 VTLITYLSLW-WFGIFNPAIVDHLGEIYSALVFGSFVFCIFLYIKGHVFPSSSDS---G 165
QY 126 LSGNLIHDWTFGIQNPQF-MGIDLK-----GMMGMLLINLSILMKSQ-DGTLSQSM 177
DB 166 SSGNVIIDFYWGMELYPRIKGFIDKVTNCRFGMMSWAVLAVTYCIKQVEMGRVADSM 225
QY 178 ILYQFPCALYITLDYFVHEEYMTSTWIIAERLGMFLVFGDLVWIPFSFSIQGWL 237
DB 226 LVNTALMIYVTRKFFWESSGYCTMDIAHADRAGFYICWGLVWVPSIYTSFGMYLVNHPV 285
QY 238 ELTP-----AAIVANCFVFLIGYVFRGANKQKHVFK-NPKAPTWGKPKVI----- 284
DB 286 NLGQALSIILLAGMLCIYINY-----DCDRQROEFRRTNGKCSWGRKAPSKI 341
QY 285 -----GKLLASGYWGIAHCHNYGLDMLALSFCGSISSPIPYFYPIYLLILIMR 340
DB 342 GETKSSLLTSGWGLSRHFVPEILSAFWTPALFDHFLPYFYVIFLTLILFDRKR 401
QY 341 DEARCAEYREINWBYRKLVPWRILPVY 369
DB 402 DDCRCSKYGYKWKYCNKVPVRIPGIY 430

RESULT 15
US-08-601-435-2
; Sequence 2, Application US/08601435
; Patent No. 5759801
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA sequence coding for a protein
; TITLE OF INVENTION: Of A, thaliana having a delta-5,7 sterol, delta-7
; TITLE OF INVENTION: reductase activity, delta-7-Red protein, production
; TITLE OF INVENTION: process, strains of transformed yeasts, uses.
; NUMBER OF SEQUENCES: 31
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/601,435
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9501723
; FILING DATE: 15-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9506517
; FILING DATE: 01-JUN-1995
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-601-435-2

Query Match 21.1%; Score 415.5; DB 1; Length 430;
Best Local Similarity 29.7%; Pred. No. 1.7e-34;
Matches 116; Conservative 78; Mismatches 153; Indels 43; Gaps 15;

QY 12 LQALTPSNNVPLLV-----GFTYLAAGSILPGKLVPGVALLDGTTRLHYCCNGLLS 65
DB 52 VOGLININWR-PTLAWKLIIFCYGFAEAILQLLPCKRVEGPISPAGNVVYKANGLAAY 110
QY 66 LLLVAL-LGIGAKMGFVSPTAISDRGLELLSTTFAPSLVTLILHFSGCKSQSKSLK 124


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Db 90 GGCTATCTTGTTGTCAGAGGAGCCAAACAAACAAACATATCTTCAAGAGAACCCCTAAA 149
QY 45 AlaProIleTPGlyLysProProLysValValGlyGlyLysLeuAlaSerGlyTyr 64
Db 150 GCTCTTATTTGGGGTAAACCTCCAAACCTGTCGGGGGGAAGTACTTGTATCTGGCTAC 209
QY 65 TrpGlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSer 84
Db 210 TGGGGAATTCGAAGCACTGCAATTATCTTGGGATATCTGCTAGCTCTTTCATTAGC 269
QY 85 LeuProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuLeu 104
Db 270 TTACCTCTGTGGAGCCAGTTCGGTGATCCCACTACTTCTACCAACATACCTGTTTTC 329
QY 105 LeuValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTyr 124
Db 330 CTGATATGGAGGAGCAAGGAGCAAGCAAGTGTCTAGAGAGTACAGAGATCTGG 389
QY 125 AlaGluTyrCysLysLeuValProTyrPheTyrProThrTyrLeuLeuLeu 140
Db 390 GTAGAATATTGCAAGCTTGTGCTTGGAGGATCTTTCCTTACGTGAT 437

RESULT 2
US-08-879-337-2
; Sequence 2, Application US/08879337B
; Patent No. 6639130
; GENERAL INFORMATION:
; APPLICANT: Jiang, Jian-Chyun
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
; FILE REFERENCE: 00786/338001
; CURRENT APPLICATION NUMBER: US/08/879,337B
; CURRENT FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/022,086
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1429
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (84)...(1189)
; NAME/KEY: variation
; LOCATION: (1)...(1429)
; OTHER INFORMATION: N can be any nucleotide.
US-08-879-337-2

Alignment Scores:
Pred. No.: 2 91e-77 Length: 1429
Score: 609.00 Matches: 107
Percent Similarity: 90.37% Conservative: 15
Best Local Similarity: 79.26% Mismatches: 13
Query Match: 80.66% Indels: 0
DB: 4 Gaps: 0

US-10-069-427-6 (1-140) x US-08-879-337-2 (1-1429)
QY 6 AsnLysValGluLeuSerLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIleGly 25
Db 786 AACAAAGTAGAAGTAAACAGTTCCTGGATTTAGTCAATTCCTTCTTGTATAGG 845
QY 26 TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysAspProLysAla 45
Db 846 TACATGGTTTTCGAGAGCTACAAACAAACAAACATATCTTTAAGAGAACCCAAACA 905
QY 46 ProIleTyrGlyLysProProLysValValGlyGlyLysLeuLeuAlaSerGlyTyr 65
Db 906 CCAATATGGGCAAGCCCTCAGTGTAGTTGGTGGAAAGTTACTGCTTTCAGGCTATTGG 965
QY 66 GlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuLeuAlaLeuSerPheSer 85
```

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Db 966 GGAATTCGAAGGCACTGTAATTACCTTGGGACCTTGATGCTGTCTCTTCAGTTG 1025
QY 86 ProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuLeu 105
Db 1026 CCATGTGGAATAAGTTCTCCGGTTCCTATATTTACCCGATATACCTTCTGATACCTATTG 1085
QY 106 ValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTyrAla 125
Db 1086 ATATGGAGAGAACCAAGAGAGAGGTTGATGTGCAGAGAGTACAGAGAGATATGGCA 1145
QY 126 GluTyrCysLysLeuValProTyrPheTyrProThrTyrLeuLeuLeuValTyr 140
Db 1146 GAGTATCTTACACTGTGCTCCCTCGAGAAATATCTTCTTATGTTTAT 1190

RESULT 3
US-08-879-337-10
; Sequence 10, Application US/08879337B
; Patent No. 6639130
; GENERAL INFORMATION:
; APPLICANT: Jiang, Jian-Chyun
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
; FILE REFERENCE: 00786/338001
; CURRENT APPLICATION NUMBER: US/08/879,337B
; CURRENT FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/022,086
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 2975
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)...(2975)
; OTHER INFORMATION: N can be any nucleotide.
US-08-879-337-10

Alignment Scores:
Pred. No.: 1 58e-60 Length: 2975
Score: 496.00 Matches: 107
Percent Similarity: 44.49% Conservative: 14
Best Local Similarity: 39.34% Mismatches: 14
Query Match: 65.70% Indels: 137
DB: 4 Gaps: 3

US-10-069-427-6 (1-140) x US-08-879-337-10 (1-2975)
QY 6 AsnLysValGluLeuSerLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIle-Gl 25
Db 2007 AACAAAGTAGAAGTAAACAGTTCCTGGATTTAGTCAATTCCTTCTTGTATAGG 2066
QY 25 Y----- 25
Db 2067 TAAGTCTGAGACATGGGTTATTTTCCATTCTTACATATCTACATAAGAAACCCACTA 2126
QY 26 -----TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLeu 40
Db 2127 TTCTCTTTGGCAGGTACATGGTTTTCGAGAGCTAACAAACAAACATATCTTTAA 2186
QY 40 sLysAspProLysAlaProIleTyrGlyLysProProLysValValGlyGlyLysLeu 60
Db 2187 GAAGAACCCAAACCAACCAATATGGGCAAGCTCCAGTGGTAGTTGGTGGAAAGTTACT 2246
QY 60 uAlaSerGlyTyrTrp----- 65
Db 2247 GGTTTCAGGCTATTTGGTATGTTATATTATCTTCTTCTTCTTCTTCTTCTTCTTCTG 2306
QY 65 ----- 65
Db 2307 TCTCTGTGTTTGTGTTCTATCATGTCGGAATAAGAGTTGAAAGTTCGCAATGACAC 2366
```


Pred. No.: 1.35e-50 Length: 572
 Score: 419.00 Matches: 73
 Percent Similarity: 96.30% Conservative: 5
 Best Local Similarity: 90.12% Mismatches: 3
 Query Match: 55.50% Indels: 0
 DB: 4 Gaps: 0

US-10-069-427-6 (1-140) x US-09-342-653-5 (1-572)

QY 60 LeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeu 79
 DB 3 CTGTATCTGGCTACTGGCGATGTCAGGACATGCAATTACCTTGGAGATCTGCTTCG 62
 QY 80 AlaLeuSerPheSerLeuProCysGlyValSerValValProTyrPheTyrProThr 99
 DB 63 GCATCTCAATCAGCTTGGCTTGGAGCCAGCTCCGTCGCTTACCGGACC 122
 QY 100 TyrLeuLeuIleLeuValLeuArgGluArgAspGluAlaArgCysSerGlnLys 119
 DB 123 TACTGTCTGATCTCTGCTGATATGGAGAGAACGAGAGAGCGAGGTCTCAGAGAG 182
 QY 120 TyrArgGluIleTrpAlaGluTyrCysLysLeuValProTyrArgIleLeuProTyrVal 139
 DB 183 TACAAGGACATCTGGCGAGAGTACTGCAAGCTTGTGCCCTGGAGGATTCTACCTTAGG 242
 QY 140 Tyr 140
 DB 243 TAC 245

RESULT 6

US-09-342-653-1

; Sequence 1, Application US/09342653

; Patent No. 6306632

; GENERAL INFORMATION:

; APPLICANT: Cahoon, Rebecca E.

; APPLICANT: Rafalski, Antoni

; TITLE OF INVENTION: Chromatin Associated Proteins

; FILE REFERENCE: BB-1118

; CURRENT APPLICATION NUMBER: US/09/342,653

; EARLIER APPLICATION NUMBER: 1999-06-29

; EARLIER FILING DATE: July 14, 1998

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 1

; LENGTH: 413

; TYPE: DNA

; ORGANISM: Zea mays

US-09-342-653-1

Alignment Scores:

Pred. No.: 1.26e-41 Length: 413
 Score: 355.00 Matches: 66
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 47.02% Indels: 0
 DB: 4 Gaps: 0

US-10-069-427-6 (1-140) x US-09-342-653-1 (1-413)

QY 75 GlyAspLeuLeuLeuAlaLeuSerPheSerLeuProCysGlyValSerValPro 94
 DB 9 GGAGACCTGCTGCTAGCATTTTGGTACGCTTGGAGTGGAGTTCGCTGCCA 68
 QY 95 TyrPheTyrProThrTyrLeuLeuIleLeuValLeuArgGluArgAspGluAla 114
 DB 69 TACTTCTACCCACGACCTGCTGCTTCTTCTGCTTCTGAGGAAAGCGGATGAGCG 128
 QY 115 ArgCysSerGlnLysTyrArgGluIleTrpAlaGluTyrCysLysLeuValProTyrArg 134
 DB 129 AGGTGCTCGAGAGTACAGGAGATCTGGCGAGAGTACTGCAAGCTCGCTCGGTGAGG 188
 QY 135 IleLeuProTyrValTyr 140

Db 189 ATCTGCTTAIGTGAC 206

RESULT 7

US-09-221-298-71/c

; Sequence 71, Application US/09221298

; Patent No. 6284241

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS

; TITLE OF INVENTION: OF COLON CANCER

; FILE REFERENCE: 210121.471

; CURRENT APPLICATION NUMBER: US/09/221,298

; CURRENT FILING DATE: 1998-12-23

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 71

; LENGTH: 428

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (281)

; OTHER INFORMATION: Where n is a, c, g or t

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (308)

; OTHER INFORMATION: Where n is a, c, g or t

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (364)

; OTHER INFORMATION: Where n is a, c, g or t

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (376)

; OTHER INFORMATION: Where n is a, c, g or t

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (383)

; OTHER INFORMATION: Where n is a, c, g or t

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (397)

; OTHER INFORMATION: Where n is a, c, g or t

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (403)

; OTHER INFORMATION: Where n is a, c, g or t

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (420)

; OTHER INFORMATION: Where n is a, c, g or t

US-09-221-298-71

Alignment Scores:

Pred. No.: 9.09e-33 Length: 428
 Score: 293.50 Matches: 57
 Percent Similarity: 63.48% Conservative: 16
 Best Local Similarity: 49.57% Mismatches: 39
 Query Match: 38.87% Indels: 3
 DB: 3 Gaps: 2

US-10-069-427-6 (1-140) x US-09-221-298-71 (1-428)

QY 29 PheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspProLysAlaProIleTrp 48
 DB 380 TTCNAGGTGCATTTTCAGAAAAAGGATTCGGGAAAAATCCCGAGTATCCAAAGCTT 321
 QY 49 Gly-----LysProProLysValValGlyLysLeu---LeuAlaSerGlyTyrTrp 65
 DB 320 GCACATTTAAAAACCATTTCATATTTCACGGGAAAAATTTTCTAGTTTCTGGATGGTGG 261
 QY 66 GlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeu 85

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Db 260 GGCTTTGTCGCCACCCCAATTAATGCTGGGTGATCTCATATGCGCTTGGCGTGCCTC 201
Qy 86 ProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuLeuLeuLeu 105
Db 200 CCATGTGGTTTAAACACCATTTCTGCCTATTCTACATAATTTATTTCCACATGTTGCTT 141
Qy 106 ValLeuArgGluArgArgAspGluAlaArgCysSerGlnLysTyrArgGluLeuTyrAla 125
Db 140 GTCCACCGAAGCTGCTGACGAGTACCACCTGTAAAGAGAATAACGGCGTGGCTTGGGAA 81
Qy 126 GluTyrCysLysLeuValProTyrArgIleLeuProTyrValTyr 140
Db 80 AAGTACTGTGAGCGTGGCGCTACCGGTATATTTCCATACATCTAC 36

RESULT 8
US-09-401-064-71/c
; Sequence 71, Application US/09401064
; Patent No. 6623923
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Mesgner, Madeline Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C2
; CURRENT APPLICATION NUMBER: US/09/401,064
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 71
; LENGTH: 428
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(428)
; OTHER INFORMATION: n = A,T,C or G
US-09-401-064-71

Alignment Scores:
Pred. No.: 9,09e-33 Length: 428
Score: 293.50 Matches: 57
Percent Similarity: 63.48% Conservative: 16
Best Local Similarity: 49.57% Mismatches: 39
Query Match: 38.87% Indels: 3
DB: 4 Gaps: 2

US-10-069-427-6 (1-140) x US-09-401-064-71 (1-428)
Qy 29 PheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspProLysAlaProIleTyr 48
Db 380 TTCNAAAGTGTCATTTTCAGAAAAGGCATTCGGGAAATTCACGATGATCCAAAGCTT 321
Qy 49 Gly-----LysProLysValValGlyLysLeu---LeuAlaSerGlyTyrTyr 65
Db 320 GCACATTTAAANCCATTCATATTTCAACGGGAAAAATTTCTAGTTTCTGGATGGTGG 261
Qy 66 GlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeu 85
Db 260 GGCATTGTGCCACCCCAATTAATTTGGTGATCTCATATGCGCTTGGCGTGGTGCCTC 201
Qy 86 ProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuLeuLeuLeu 105
Db 200 CCATGTGGTTTAAACACCATTTCTGCCTATTCTACATAATTTATTTCCACATGTTGCTT 141
Qy 106 ValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluLeuTyrAla 125
Db 140 GTCCACCGAAGCTGCTGACGAGTACCACCTGTAAAGAGAATAACGGCGTGGCTTGGGAA 81
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Qy 126 GluTyrCysLysLeuValProTyrArgIleLeuProTyrValTyr 140
Db 80 AAGTACTGTGAGCGTGGCGCTACCGGTATATTTCCATACATCTAC 36

RESULT 9
US-08-439-131A-1
; Sequence 1, Application US/08439131A
; Patent No. 5512472
; GENERAL INFORMATION:
; APPLICANT: Lai, Margaret H. K.
; APPLICANT: Bard, Martin
; APPLICANT: Kirsch, Donald R.
; TITLE OF INVENTION: A DNA Sequence Encoding Sterol Delta
; Patent No. 5512472
; TITLE OF INVENTION: Reductase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,131A
; FILING DATE: 11-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/107,347
; FILING DATE: 16-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 854-012 (32,141)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2528 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 419..1732
US-08-439-131A-1

Alignment Scores:
Pred. No.: 1.16e-25 Length: 2528
Score: 252.50 Matches: 53
Percent Similarity: 56.12% Conservative: 25
Best Local Similarity: 38.13% Mismatches: 48
Query Match: 33.44% Indels: 13
DB: 1 Gaps: 2

US-10-069-427-6 (1-140) x US-08-439-131A-1 (1-2528)
Qy 8 ValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIleGlyTyrLeu 27
Db 1337 GTGGAATTGGGATGGGTGAAAGTTCGCGTATATTAGCCATAATGTTTTGGGTTTCCAC 1396
Qy 28 ValPheArgGlyValAsnLysGlnLysHisValPheLysLysAspProLysAlaProIle 47
```

1397 ATCTTCACCTCGCAATAAGCAAAAATCTGAGTTTAGACAA-----1433

48 TtpGlyLysProPolysValVal-----GlyGlyLysLeuLeuAla 61

1439 ---GGTAAATTAGAAAATCTTAAAAAAGATTTCAGACAAAGCGTGGTACAAAGTTATTATGT 1495

62 SerGlyTyrTrpGlylleAlaArgHIScysAsnTyrLeuGlyAspLeuLeuAlaLeu 81

1496 GACGGGTGGTGGGCTAAATCACAGCATATCAATTACTTTGGCGATTGGCTGATTCATTATTA 1555

82 SerPheSerLeuProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeu 101

1556 AGTTGGTGTGTGGCCACCTGGTTCCAAACCTCCCTTGACATATTACTACTCGTTGTACTTC 1515

102 LeulleLeuValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArg 121

1616 GCCACGTGTGTTATTACACCGTCAACACGTGATGAGCAAGTGGCGCTGAAATATGGC 1675

122 GluileTrpAlaGlyTyrCysLysLeuValProTyrArgIleLeuProTyrValTyr 140

1676 GAAATTTGGAGAAATACGAAGAAAAGTTCCTTACAGATCAATTCATATGTTTAT 1732

RESULT 10

US-08-440-674-1

; Sequence 1, Application US/08440674

; Patent No. 5525496

; GENERAL INFORMATION:

; APPLICANT: Margaret H. Lai

; TITLE OF INVENTION: A DNA Sequence Encoding Sterol

; Patent No. 5525496

; TITLE OF INVENTION: 14

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSER: American Cyanamid Company

; STREET: One Cyanamid Plaza

; CITY: Wayne

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07470

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" 1.44 Mb diskette

; COMPUTER: IBM PC

; OPERATING SYSTEM: MS DOS

; SOFTWARE: Word Processor

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/440,674

; FILING DATE: May 15, 1995

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/107,347

; FILING DATE: August 16, 1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Alan M. Gordon

; REGISTRATION NUMBER: 30637

; REFERENCE/DOCKET NUMBER: 854-P0012 Div (32,141)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-831-3244

; TELEFAX: 201-831-3305

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2528 bases and 438 amino acids

; TYPE: nucleic acid and amino acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE:

; DESCRIPTION: DNA encoding a polypeptide

; FRAGMENT TYPE: entire sequence

; IMMEDIATE SOURCE: Saccharomyces cerevisiae

; IMMEDIATE SOURCE: clone

; FEATURE:

; OTHER INFORMATION: sterol 14 reductase gene,

; OTHER INFORMATION: translated

```
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 2528 bases
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
; MOLECULE TYPE:
;   DESCRIPTION: DNA encoding a polypeptide
; FRAGMENT TYPE: entire sequence
; IMMEDIATE SOURCE: Saccharomyces cerevisiae
; IMMEDIATE SOURCE: clone
; FEATURE:
;   OTHER INFORMATION: sterol delta 14 reductase gene,
;   OTHER INFORMATION: translated polypeptide and flanking DNA
US-08-107-348-1
Alignment Scores:
Pred. No.: 1,16e-25 Length: 2528
Score: 252.50 Matches: 53
Percent Similarity: 56.12% Conservative: 25
Best Local Similarity: 38.13% Mismatches: 48
Query Match: 33.44% Indels: 13
DB: 1 Gaps: 2
US-10-069-427-6 (1-140) x US-08-107-348-1 (1-2528)
Qy 8 ValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuLeuGlyTyrLeu 27
Db 1337 GTGGAATTGGATGGTGGAAAGTTGTCGGTATATTAGCCATAATGTTTTTGGGTTCAC 1396
Qy 28 ValPheArgGlyAlaLeuLysGlnLysHisValPheLysAspProLysAlaProIle 47
Db 1397 ATCTTCCACTCGGCAATAAGCAAAATCTGAGTTAGACAA-----GlyGlyLysLeuAla 1438
Qy 48 TrpGlyLysProLysValVal-----GlyGlyLysLeuAla 61
Db 1439 --GGTAAATTAGAAATCTAAAGAGTATTCAGACAAAGCGTGGTACAAAGTTATTATGT 1495
Qy 62 SerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeu 81
Db 1496 GACGGGTGGTGGGCTAAATCACAGCATATCAATTTACTTTCGGCATTTGGCTGATTCATTA 1555
Qy 82 SerPheSerLeuProCysGlyValSerSerValValProTyrPheTyrProTyrLeu 101
Db 1556 AGTGGTGGTGGCCACTGGTCCAAACTCCCTTGACATATTACTACTCGTTGTACTTC 1615
Qy 102 LeuLeuLeuValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArg 121
Db 1616 GCCACGTTGTTATTACACCGCTCAACAACGTGATGAGCACAAGTCCGCTGAAATATGGC 1675
Qy 122 GluIleTrpAlaGluTyrCysLysLeuValProTyrArgIleLeuProTyrValTyr 140
Db 1676 GAAATTCGGNAGATAGCAAGAAAGTTCCITCAAGATCATTCATATGTTAT 1732
RESULT 12
US-09-443-041A-21
; Sequence 21, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO: 21
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-443-041A-17
Alignment Scores:
Pred. No.: 4.44e-25 Length: 1870
Score: 1870.00 Matches: 53
Percent Similarity: 59.15% Conservative: 31
Best Local Similarity: 37.32% Mismatches: 38
Query Match: 33.11% Indels: 20
DB: 4 Gaps: 6
US-10-069-427-6 (1-140) x US-09-443-041A-21 (1-1695)
Qy 12 LeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuLeuGlyTyrLeuValPheArgGly 31
Db 1016 CTTCTAGCTGGAATG-----TTGTGCATATAC---ATAAACTAT-----GAT 1054
Qy 32 AlaAsnLysGlnLysHisValPheLysLys---AspProLysAlaProIleTrpGlyLys 50
Db 1055 TGTGACCTGTGACGCCAAGAAATTTTCGACGACGAATGGGAAATGCTCGTCTGGGGCAAG 1114
Qy 51 ---ProProLysValValGly-----GlyLys 58
Db 1115 GCTCCATCTAAGATTGTTGCCTCTTATCAGACTACAAAGCGGAGAAACTAAACCAAGTCTT 1174
Qy 59 LeuLeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeu 78
Db 1175 CTTCTGACTTCTGGATGTGGGGCTTGTACGTCACATCTCCACTATGTCCCAGAGATACTA 1234
Qy 79 LeuAlaLeuSerPheSerLeuProCysGlyValSerSerValValProTyrPheTyrPro 98
Db 1235 TCTGCATTTTCTGACGTGTTCCAGCTCTTTTCATCATCTTCTTACCATACTTCTACGTG 1294
Qy 99 ThrTyrLeuLeuLeuLeuValLeuArgGluArgAspGluAlaArgCysSerGln 118
Db 1295 ATCTTTCTGACTATATTATTGTTTTCACCGAGCAAGAGGATGATGACCGGTGCTCATCA 1354
Qy 119 LysTyrArgGluIleTrpAlaGluTyrCysLysLeuValProTyrArgIleLeuProTyr 138
Db 1355 AAGTACGGAGAGTACTGGAAGATTTCATGCAACAAAGTACCATACAGAGTCACTTCTCGGC 1414
Qy 139 ValTyr 140
Db 1415 ATTTAC 1420
RESULT 13
US-09-443-041A-17
; Sequence 17, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO: 17
; LENGTH: 1870
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-443-041A-17
Alignment Scores:
Pred. No.: 4.44e-25 Length: 1870
Score: 1870.00 Matches: 53
Percent Similarity: 59.15% Conservative: 31
Best Local Similarity: 37.32% Mismatches: 38
Query Match: 33.11% Indels: 20
DB: 4 Gaps: 6
```

Score: 247.00 Matches: 54
 Percent Similarity: 57.75% Conservative: 28
 Best Local Similarity: 38.03% Mismatches: 40
 Query Match: 32.72% Indels: 20
 DB: 4 Gaps: 6

US-10-069-427-6 (1-140) x US-09-443-041A-17 (1-1870)

Qy 12 LeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIleGlyTyrLeuValPheArgGly 31
 Db 1005 CTCCTGCTGGAATA-----TTGTGCATATAT---ATAACTAT-----GAC 1043
 Qy 32 AlaAsnLysGlnLysHisValPheLysLys---AspProLysAlaProIleTyrGlyLys 50
 Db 1044 TGTGATCGTCAGCGCCCAAGAAATCCGTCGACAAATGGGAAATGCTCAATATATGGGCAAA 1103
 Qy 51 ---ProProLysValVal-----GlyGlyLys 58
 Db 1104 GCTCCATCTAAGATTGTTGCTTCTATCAGACTACAAATGGAGAAACAAAAGCAGCTTT 1163
 Qy 59 LeuLeuAlaSerGlyTyrTyrGlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeu 78
 Db 1164 CTCCTGATCTCTGATGCGGGCTGTCTCGTCATTTTCCATATGTTCCAGAGATTCTA 1223
 Qy 79 LeuAlaLeuSerPheSerLeuProCysGlyValSerValValProTyrPheTyrPro 98
 Db 1224 TCCTGCTTTTCTGGACAGTTCAGCTCTTTTGATCATTTCTGCGGTACTTCTATGTG 1283
 Qy 99 ThrTyrLeuLeuLeuLeuValLeuArgGluArgAspGluAlaArgCysSerGln 118
 Db 1284 ATCTTTCTGACCATATTGCTGTTCGACCGAGTAAAGGGATGATGACCGAGTCTCATCA 1343
 Qy 119 LysTyrArgGluIleTyrAlaGluTyrCysLysLeuValProTyrPheArgIleLeuProTyr 138
 Db 1344 AGTATGGCAAGTATGGAAAGATGCTACTGCAACAAAGTCCGTCGAGGTTATTCCTGCGC 1403
 Qy 139 ValTyr 140
 Db 1404 ATTTAC 1409

RESULT 14

US-09-443-041A-19
 ; Sequence 19, Application US/09443041A
 ; Patent No. 6465717
 ; GENERAL INFORMATION:
 ; APPLICANT: Famodu, Omolayo O.
 ; APPLICANT: Orozco, Buddy
 ; APPLICANT: Rafalski, Antoni
 ; APPLICANT: Shen, Jennie
 ; TITLE OF INVENTION: Sterol Metabolism Enzymes
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/443,041A
 ; PRIOR FILING DATE: 1999-11-18
 ; PRIOR FILING DATE: 60/109,283
 ; PRIOR FILING DATE: 1998-11-20
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 19
 ; LENGTH: 1646
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 US-09-443-041A-19

Alignment Scores:
 Pred. No.: 1.16e-24 Length: 1646
 Score: 243.50 Matches: 54
 Percent Similarity: 58.11% Conservative: 32
 Best Local Similarity: 36.49% Mismatches: 41
 Query Match: 32.25% Indels: 21
 DB: 4 Gaps: 7

US-10-069-427-6 (1-140) x US-09-443-041A-19 (1-1646)

Qy 7 LysValGluLeuSerLeuLeu---SerGlyLeuAlaAsnLeuCysIlePheLeuIleGly 25
 Db 932 AAGCTAGCGCTCTCAATTTTAGTAGCTGGCATT-----CTTTGCATATAC---ATCAAC 982
 Qy 26 TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysLys---AspProLys 44
 Db 983 TAT-----GATTGTGACGCGCAAGCAAGAAATTTCTGAGGACAAATGGAATA 1030
 Qy 45 AlaProIleTyrGlyLysProLysValVal-----GlyGly 57
 Db 1031 GGCACAGCTCGGGGAAAAGCTCTTCAAAGATAGAGGCCACATATACTACTTCTGCGG 1090
 Qy 58 Lys-----LeuLeuAlaSerGlyTyrTyrGlyIleAlaArgHisCysAsn 72
 Db 1091 GAAACTAAAGAACCCCTCTTTTAACTCTGGATGGTGGGGATTATCTCGTCACTTTTCAT 1150
 Qy 73 TyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeuProCysGlyValSerVal 92
 Db 1151 TATGTCCTGAAATACTGGCAGCTTTCTTCTGGACAGTCCCGAGCTCTTTTCGAACATTTT 1210
 Qy 93 ValProTyrPheTyrProTyrTyrLeuLeuIleLeuValLeuArgGluArgAsp 112
 Db 1211 TTGCTTACTTCTACGTGATATTTTACCATCTCTTCTTGTATCGACAAACCGAGAT 1270
 Qy 113 GluAlaArgCysSerGlnLysTyrArgGluIleTyrAlaGluTyrCysLysLeuValPro 132
 Db 1271 GATGATCGTTGCAGATCCAGATGCGCAAGTACTGGAACTATATTCGACAAAGGTACCT 1330

RESULT 15

US-08-879-337-23
 ; Sequence 23, Application US/08879337B
 ; Patent No. 6639130
 ; GENERAL INFORMATION:
 ; APPLICANT: Jang, Jyan-Chyun
 ; APPLICANT: Sheen, Jen
 ; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
 ; FILE REFERENCE: 00786/338001
 ; CURRENT APPLICATION NUMBER: US/08/879,337B
 ; CURRENT FILING DATE: 1997-06-20
 ; EARLIER APPLICATION NUMBER: 60/022,086
 ; EARLIER FILING DATE: 1996-06-21
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 23
 ; LENGTH: 221
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-08-879-337-23

Alignment Scores:
 Pred. No.: 1.13e-24 Length: 221
 Score: 234.00 Matches: 41
 Percent Similarity: 90.20% Conservative: 5
 Best Local Similarity: 80.39% Mismatches: 5
 Query Match: 30.99% Indels: 0
 DB: 4 Gaps: 0

US-10-069-427-6 (1-140) x US-08-879-337-23 (1-221)

Qy 90 SerSerValValProTyrPheTyrProTyrLeuLeuIleLeuValLeuArgGlu 109
 Db 1 AGTTCTCCGGTTCATATTTCTACCCGATATATCTTCTGATCTATTGATATGAGAGAA 60
 Qy 110 ArgArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTyrAlaGluTyrCysLys 129
 Db 61 CGAAGACCGAGGTTCGATGTGACAGAGAGTACAGAGATATGGCAGAGTATCTAGA 120
 Qy 130 LeuValProTyrPheArgIleLeuProTyrValTyr 140

Db 121 CTTGTCCCTGGAGATACTTCTTANGTTTAT 153

Search completed: June 14, 2004, 12:20:38
Job time : 45.8821 secs

[The body of the document contains extremely faint, illegible text that appears to be bleed-through from the reverse side of the page. No specific content can be transcribed.]

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2004, 09:48:07 ; Search time 601.709 Seconds
(without alignments)
2605.220 Million cell updates/sec

Title: US-10-069-427-8
Perfect score: 1965
Sequence: 1 MESHVDLGLFLQALTPSWN.....REINAEYKLVFWRILPVYV 369

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 segs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=N Geneseq 29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10069427 @CGN 1.1 586 @runat_14062004_104800_24751 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 29Jan04:.*
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2: Geneseqn19808:.*
3: Geneseqn2000s:.*
4: Geneseqn2000s:.*
5: Geneseqn2000s:.*
6: Geneseqn2000s:.*
7: Geneseqn2003as:.*
8: Geneseqn2003bs:.*
9: Geneseqn2003cs:.*
10: Geneseqn2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1965	100.0	1364	4 AAF30677	Aaf30677 Soybean s
2	1946.5	99.1	1631	4 AAF30675	Aaf30675 Corn ster
3	1569.5	79.3	1423	2 AA04237	Aav04237 Arabidops
4	1568.5	79.8	1110	3 AAC45795	Aac45795 Arabidops
5	1568.5	79.8	1380	3 AAC37623	Aac37623 Arabidops
6	990.5	50.4	6588	2 AA04238	Aav04238 Arabidops
7	973	49.5	625	9 ADD17001	Add17001 DNA (Seq
8	706	35.9	427	4 AAF30674	Aaf30674 Soybean s

9	630	32.1	3714	6 ABK35567	ABK35567 Gene LBR
10	630	32.1	3714	6 ABK83864	ABK83864 Human cDN
11	621	31.6	667	4 AAF30676	AAF30676 Soybean s
12	594.5	30.3	1347	6 AB232373	AB232373 Candida s
13	547.5	27.9	2528	2 AAQ89202	Aaq89202 Sterol-de
14	547.5	27.9	2528	2 AAT32142	Aat32142 Saccharom
15	547.5	27.9	2528	2 AAT30357	Aat30357 Saccharom
16	544.5	27.7	1546	6 ABQ54166	ABQ54166 Human ova
17	523.5	26.6	2481	2 AAX90448	Aax90448 Human sec
18	523.5	26.6	2481	2 AAS59277	Aas59277 Human cDN
19	523.5	26.6	2481	6 ABA90946	ABA90946 Human pol
20	523.5	26.6	2652	2 AAX23387	Aax23387 Human del
21	523.5	26.6	2652	2 AAX23386	Aax23386 Human del
22	522	26.6	2427	9 ADB58439	ADB58439 Toxicity-
23	514.5	26.6	2427	9 ADB53021	ADB53021 Primary r
24	514.5	26.2	1875	9 ADD69664	Add69664 Human REM
25	512	26.1	1494	7 ABT20861	ABT20861 Aspergill
26	499.5	25.4	1614	7 ABT20263	ABT20263 Aspergill
27	498.5	25.4	3614	7 ABT19667	ABT19667 Aspergill
28	490.5	25.0	1896	4 AAF28559	AAF28559 DNA encod
29	466.5	23.7	3242	7 ABT17853	ABT17853 Aspergill
30	451.5	23.0	1245	7 ABT19041	ABT19041 Aspergill
31	443.5	22.6	1646	7 ABX15830	ABX15830 cDNA enco
32	441.5	22.5	1695	7 ABX15831	ABX15831 cDNA enco
33	439	22.3	800	9 ADD16149	Add16149 cDNA (Seq
34	434.5	22.1	1299	6 ABZ14307	ABZ14307 Arabidops
35	434.5	22.1	1501	3 AAC51344	AAC51344 Arabidops
36	434.5	22.1	1531	6 ABQ82663	ABQ82663 Arabidops
37	434	22.1	1870	7 ABX15829	ABX15829 cDNA enco
38	432.5	22.0	1336	3 AAC40077	Aac40077 Arabidops
39	415.5	21.1	1496	2 AAT39358	Aat39358 Arabidops
40	413	21.0	1181	9 ADE07087	Ade07087 Novel cod
41	311.5	15.9	476	9 ADB56005	ADB56005 Toxicity-
42	289	14.7	1242	7 ABT18447	ABT18447 Aspergill
43	280	14.2	458	6 ABA94581	ABA94581 Gene #107
44	274.5	14.0	428	3 AAA77792	AAA77792 cDNA enco
45	274.5	14.0	428	4 AAI28530	AAI28530 Colon tum

ALIGNMENTS

RESULT 1
AAF30677
ID AAF30677 standard; cDNA; 1364 BP.
XX
AC AAF30677;
XX
DT 11-JUN-2001 (first entry)
XX
DE Soybean sterol delta-14 reductase clone ssm.pk0031.d12.fis.
XX
KW Soybean sterol delta-14 reductase; transgenic plant; herbicide;
KW fungicide; ss.
XX
OS Glycine max.
XX
FH Key Location/Qualifiers
FT CDS 64..1173
FT /*tag= a
FT /partial
XX
PN WO200123539-A2.
XX
PD 05-APR-2001.
XX
PF 27-SEP-2000; 2000WO-US026442.
XX
PR 30-SEP-1999; 99US-0156820P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Fancdu OO, Kinney AJ;
XX

DR WPI; 2001-266146/27.
 XX P-PSDB; AAB20381.
 PT Novel gene encoding sterol delta-14 reductase useful for transgenic plant
 PT production with altered sterol delta-14 reductase.
 XX Claim 7; Page 39; 45pp; English.
 PS
 XX The present sequence is that of the full insert sequence of clone
 CC sm.p0031.d12, which includes a full-length coding region for soybean
 CC sterol delta-14 reductase (see AAB20381). The clone was isolated from a
 CC soybean shoot meristem cDNA library, following homology searches. The
 CC predicted protein shows amino acid sequence homology to Arabidopsis
 CC thaliana and Ascoebolus immersus sterol delta-14 reductases. The invention
 CC relates to isolated polynucleotides encoding sterol delta-14 reductases
 CC and to transgenic plants comprising such polynucleotides. It also relates
 CC to the construction of a chimeric gene encoding all or a portion of the
 CC sterol delta-14 reductase, in sense or antisense orientation, where
 CC expression of the chimeric gene results in production of altered levels
 CC of the enzyme in a transformed host cell. The availability of plant
 CC sterol delta-14 reductase genes will provide a means of altering sterol
 CC production and/or composition of plants, to identify compounds that may
 CC be useful as novel herbicides and fungicides, and to identify mutants of
 CC these genes that are resistant to these herbicides and will enable the
 CC production of herbicide-resistant crops
 XX
 SQ Sequence 1364 BP; 346 A; 277 C; 296 G; 445 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3,22e-200 Length: 1364
 Score: 1965.00 Matches: 369
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-10-069-427-8 (1-369) x AAF30677 (1-1364)

QY 1 MetMetGluSerHisValAspLeuGlyPheLeuLeuGlnAlaLeuThrProSerTrpAsn 20
 DB 64 ATGATGAGTCACACGTGGATCTAGGTTTCCTTCAAGCTCTCACTTCCTTGGAC 123
 QY 21 SerValProLeuLeuValGlyPhePheThrTyrrLeuAlaValAlaGlySerIleLeuPro 40
 DB 124 TCCGTTCCCTTGGTTCGGGTTCTTCACTTACTTGGCGGTTGCTGGATCCATCTCCCT 183
 QY 41 GlyLeuLeuValProGlyValAlaLeuLeuAspGlyThrArgLeuHisTyrrCysAsn 60
 DB 184 GGAAACCTTCTCCTGGCGTTGACACTCGATGGAACCTGCTACACTATTGCTGCAAT 243
 QY 61 GlyLeuLeuSerLeuLeuLeuValAlaLeuLeuGlyIleGlyAlaLysMetGlyPhe 80
 DB 244 GGCTGCTCTCGCTTCTCTGTTGTTGTCATCTTCCGGATCGGTCCCAAGATGGTTTT 303
 QY 81 ValSerProThrAlaIleSerAspArgGlyLeuGluLeuLeuSerThrThrPheAlaPhe 100
 DB 304 GTGCTCTCCCACTCCATATACAGACAGAGACTGAGCTGTGTCACAACTTTGCTTTC 363
 QY 101 SerPheLeuValThrLeuLeuLeuHisPheSerGlyCysLysSerGlnSerLysGlySer 120
 DB 364 AGTTTCTTGTAACTTGATATGCAATTTTCCGGTTGCAAGTCACAAAGTAAGTTCA 423
 QY 121 SerLeuLysProHisLeuSerGlyAsnLeuLeuHisAspTrpThrPheGlyIleGlnLeu 140
 DB 424 TCACATAAGCCTCATCTCAGTGAACCTGATACAGCATTTGGTGGTTGGTATACAACTA 483
 QY 141 AsnProGlnPheMetGlyIleAspLeuLysAlaGlyMetMetGlyTrpLeuLeuLeuAsn 160
 DB 484 AATCCACAGTTTCATGGGTATCGACCTCAAGCTGGAATGATGGATGGCTACTTATCAT 543
 QY 161 LeuSerIleLeuMetLysSerIleGlnAspGlyThrLeuSerGlnSerMetIleLeuTyrr 180
 DB 544 TTATCTATTCTTATGAAGACATTCAGATGGTACTTTGAGCCAGTCAATGATCTCTAC 603

QY 181 GlnLeuPheCysAlaLeuTyrrIleLeuAspTyrrPheValHisGluGluTyrrMetThrSer 200
 DB 604 CAGCTATTCTGTGCATATACATCCTGGACTATTTTGTACATGAAGAGTACATGACATCC 663
 QY 201 ThrTrpAspIleIleAlaGluArgLeuGlyPheMetLeuValPheGlyAspLeuValTrp 220
 DB 664 ACTGGGACATATTTGCAGAGAGACTGGGCTTCATGTTGGTCTTTGGAGATTAGTGTG 723
 QY 221 IleProPheSerPheSerIleGlnGlyTrpTrpLeuLeuMetAsnSerValGluLeuThr 240
 DB 724 ATTCCTTCTCTTTCAGCATACAGGATGGTGCTCTTGTATGAACAGTGTGGAGTTAACA 783
 QY 241 ProAlaIleValAlaAsnCysPheValPheLeuIleGlyTyrrMetValPheArgGly 260
 DB 784 CCAAGTCCCATTTAGCTAATTCCTTTGGTTCCTGATTTGGATGATCATGGTATTTCAGGA 843
 QY 261 AlaAsnLysGlnLysHisValPheLysLysAsnProLysAlaProIleTrpGlyLysPro 280
 DB 844 GCRAACCAAGCAAAAGCATGTGTTCAAAAGAAATCCAAAGGCTCCTATCTGGGTAAGCCT 903
 QY 281 ProLysValIleGlyLysLeuLeuAlaSerGlyTyrrTrpGlyIleAlaArgHisCys 300
 DB 904 CCAAAAGTCAATTTGGTGAAGACTACTGCTTCTGGTTATTGGGGTATTGCTAGACTGT 963
 QY 301 AsnTyrrLeuGlyAspLeuMetLeuAlaLeuSerPheSerLeuProCysGlyIleSerSer 320
 DB 964 AATTACCTAGGGATTTGATGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1023
 QY 321 ProIleProTyrrPheTyrrProIleTyrrLeuLeuIleLeuIleTrpArgGluArgThr 340
 DB 1024 CCAATTCCTACTTCTATCCAAATTTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1083
 QY 341 AspGluAlaArgCysAlaGluLysTyrrArgGluIleTrpAlaGluTyrrArgLysLeuVal 360
 DB 1084 GATGAAGCTCGTTGGCGCGAGAGATAGAGAGATATGGCCCGAGTATCGTAAACTTGT 1143
 QY 361 ProTrpArgIleLeuProTyrrValTyrr 369
 DB 1144 CCATGGAGAATATTGCCTTACGTTTAT 1170

RESULT 2
 AAF30675
 ID AAF30675 standard; cDNA; 1631 BP.
 XX AAF30675;
 AC AAF30675;
 XX 11-JUN-2001 (first entry)
 DT
 DE Corn sterol delta-14 reductase clone p0097.cqrau67ra.fis.
 KW Corn; maize; sterol delta-14 reductase; transgenic plant; herbicide;
 KW fungicide; ss.
 OS Zea mays.
 FH Key Location/Qualifiers
 FT CDS 74..1198
 FT /*tag= a
 PN WO200123539-A2.
 PD 05-APR-2001.
 XX 27-SEP-2000; 2000WO-US026442.
 PF 30-SEP-1999; 99US-0156820P.
 PR (DUPO) DU PONT DE NEMOURS & CO E I.
 PA Famodu OO, Kinney AJ;
 PI WPI; 2001-266146/27.
 DR

DR P-PSDB; AAB20379.
 XX Novel gene encoding sterol delta-14 reductase useful for transgenic plant
 PT production with altered sterol delta-14 reductase.
 XX
 PS Claim 7; Page 36; 45pp; English.
 XX

CC The present sequence is that of the full-insert sequence of clone
 CC p0097.cgrau67ra:fls, coding for corn sterol delta-14 reductase (see
 CC AAB20379). The clone was isolated from a cDNA library prepared from corn
 CC V9 whorl section + ECB1, following database homology searches. The
 CC predicted polypeptide shows amino acid sequence homology to Arabidopsis
 CC thaliana and Asobolus imneisus sterol delta-14 reductases. The invention
 CC relates to isolated polynucleotides encoding sterol delta-14 reductases
 CC and to transgenic plants comprising such polynucleotides. It also relates
 CC to the construction of a chimeric gene encoding all or a portion of the
 CC sterol delta-14 reductase, in sense or antisense orientation, where
 CC expression of the chimeric gene results in production of altered levels
 CC of the enzyme in a transformed host cell. The availability of plant
 CC sterol delta-14 reductase genes will provide a means of altering sterol
 CC production and/or composition of plants, to identify compounds that may
 CC be useful as novel herbicides and fungicides, and to identify mutants of
 CC these genes that are resistant to these herbicides and will enable the
 CC production of herbicide-resistant crops

XX Sequence 1631 BP; 392 A; 330 C; 353 G; 556 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,99e-198 Length: 1631
 Score: 1946.50 Matches: 368
 Percent Similarity: 98.40% Conservative: 0
 Best Local Similarity: 98.40% Mismatches: 1
 Query Match: 99.06% Indels: 5
 DB: 4 Gaps: 1

US-10-069-427-8 (1-369) x AAF30675 (1-1631)

QY 1 MetMetGluSerHisValAspLeuGlyPheLeuLeuGluAlaLeuThrProSerTrpAsn 20
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 QY 21 SerValProLeuLeuValGlyPhePheThrTyrrLeuAlaValAlaGlySerLeuPro 40
 DB 134 TCGGTTCTCTGCTTGGTGGGTTCTTCACTTACTTGGCCGTTGCTGGATCCATTCCT 193
 QY 41 GlyLysLeuValProGlyValAlaLeuLeuAspGlyThrArgLeuHisTyrrCysAsn 60
 DB 194 GGAACACTGTTCTTGGCGTTGGCACTACTCGATGGAACTCGTCTACACTATTGCTGCAT 253
 QY 61 GlyLeuLeuSerLeuLeuLeuValAlaLeuLeuGlyIleGlyAlaLysMetGlyPhe 80
 DB 254 GGTCTGCTCTCGCTTCTTCTGTTGGTTGGCACTTCTCGGATCGGTGCCAAGATGGGTTT 313
 QY 81 ValSerProThrAlaIleSerAspArgGlyLeuGluLeuSerThrThrPheAlaPhe 100
 DB 314 GTGCTCTCCCACTGCCATATCAGACAGAGCACTTGAGCTGCTGCTGCCAACTTTGCTTC 373
 QY 101 SerPheLeuValThrLeuLeuLeuHisPheSerGlyCysLysSerGlnSerLysGlySer 120
 DB 374 AGTTTCTTGTAACTGATATTGCACTTTTCCGGTTGCAAGTCACAAAGTAAAGTTCA 433
 QY 121 SerLeuLysProHisLeuSerGlyAsnLeuLeuHisAspTrpThrPheGlyIleGlnLeu 140
 DB 434 TCACTAAAGCCTCATCTCAGTGGAAACCTGATACACGATTTGGTGGTTGGTATACAACTA 493
 QY 141 AsnProGlnPheMetGlyIleAspLeuLys-----AlaGlyMetMetGly 155
 DB 494 AATCCACAGTTTCATGGTATCGACCTCAATTTTCTTTGTTAGAGCTGATGATGGA 553
 QY 156 TrpLeuLeuLeuAsnLeuSerIleLeuMetLysSerIleGlnAspGlyThrLeuSerGln 175
 DB 554 TGGCTACTTATCAATTTATCTATTCTTATGAAGAGCATTCAGATGGTACTTTTGAGCCAG 613

QY 176 SerMetIleLeuTyrGlnLeuPheCysAlaLeuTyrIleLeuAspTyrPheValHisGlu 195
 DB 614 TCAATGATCTCTACCACTATTCTGTGCATATACATCTCTGGACTATTTTGTACATGAA 673
 QY 196 GluTyrMetThrSerThrTrpAspIleIleAlaGluArgLeuGlyPheMetLeuValPhe 215
 DB 674 GAGTACATGACATCCACCTGGGACATATTGCAGAGAGACTGGGCTTCATGTTGTCTTT 733
 QY 216 GlyAspLeuValTrpIleProPheSerPheSerIleGlnGlyTrpTrpLeuLeuMetAsn 235
 DB 734 CGAGATTAGTGTGGATTCCTTCTCTTACGATACAGGATGGTGGCTCTCTGATGAAC 793
 QY 236 SerValGluLeuThrProAlaAlaIleValAlaAsnCysPheValPheLeuIleGlyTyr 255
 DB 794 AGTGGGAGTTAAACACAGCTGCCATTGTAGCTTAATGCTTGTGTTCTCTGATTGGATAC 853
 QY 256 MetValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAsnProLysAlaPro 275
 DB 854 ATGGTATTTCGAGGAGCAACAAGCAATGTTTCAAAAAGAAATCCAAAGGCTCCT 913
 QY 276 IleTrpGlyLysProProLysValIleGlyLysLeuLeuAlaSerGlyTyrTrpGly 295
 DB 914 ATCTGGGTAAAGCCTCCAAAAGTCATTGGTGGAAAGCTACTTGTCTCTGTTATTGGGGT 973
 QY 296 IleAlaArgHisCysAsnTyrLeuGlyAspLeuMetLeuAlaLeuSerPheSerLeuPro 315
 DB 974 ATTGCTAGACACTGTAATTACTAGGGGATTTGATGCTTCTCTCTCTCTTAGCTTACCA 1033
 QY 316 CysGlyIleSerSerProIleProTyrPheTyrProIleTyrLeuLeuLeuLeuLeu 335
 DB 1034 TGTGGATAAGTTCACCAATTCCTACTTCTTATCCAATTTATCTTCTTATCTCTTATC 1093
 QY 336 TrpArgGluArgThrAspGluAlaArgCysAlaGluLysTyrArgGluIleTrpAlaGlu 355
 DB 1094 TGGAGAGAGAGAGGATGAAGCTCGTTGCCCGAGAGATATAGAGAGATATGGCCGAG 1153
 QY 356 TyrArgLysLeuValProTrpArgIleLeuProTyrValTyr 369
 DB 1154 TATGTAACATTGTTCCATGGAGAATATTGCTTACGTTTAT 1195
 RESULT 3
 AAV04237
 ID AAV04237 standard; cDNA; 1429 BP.
 XX
 AC AAV04237;
 DT 22-JUN-1998 (first entry)
 XX
 DE Arabidopsis C-14 sterol reductase cDNA clone D13.
 XX
 KW C-14 sterol reductase; ELL gene; transgenic plant; steroid;
 KW crop improvement; ds.
 XX
 OS Arabidopsis thaliana.
 XX
 FH Key Location/Qualifiers
 CDS 84..1193
 FT /*tag= a
 XX
 PN WO9748793-A1.
 XX
 PD 24-DEC-1997.
 XX
 PF 20-JUN-1997; 97WO-US010644.
 XX
 PR 21-JUN-1996; 96US-0022086P.
 XX
 PA (GEO) GEN HOSPITAL CORP.
 XX
 PI Jang J, Sheen J;
 XX WPI; 1998-063134/06.
 DR P-PSDB; AAW41576.
 DR

XX New isolated plant C-14 sterol reductase gene - used to develop products
 PT for the genetic manipulation of a plant sterol biosynthetic pathway to
 PT improve plant characteristics.

XX Claim 7; Fig 14; 7lpp; English.

XX cDNA clone D13 includes a coding region for a novel C-14 sterol reductase
 CC (see AA041576) of Arabidopsis thaliana. An Arabidopsis mutant, ell (extra
 CC long life), that displayed a life span that was at least 3 times greater
 CC than wild-type plants, was isolated. The ell mutant was isolated by T-DNA
 CC tagging, and used to screen cDNA and genomic libraries from a wild-type
 CC plant to identify clone D13 and a 6588 bp genomic clone (see AA04238). A
 CC pure plant C-14 sterol reductase (C14SR) is claimed, as are purified using
 CC encoding C14SR, a vector, a method of producing recombinant C14SR using
 CC transformed plant cells, a transgenic plant that expresses C14SR DNA and
 CC a seed or cell from such a plant, and methods for detecting and isolating
 CC a C14SR gene, and for reducing the level of C14SR in a transgenic plant
 CC using an antisense construct. The genetic manipulation of plant sterol
 CC composition is useful for improving food quality and oil stability, and
 CC for regulating the formation of compounds having anti-nutritional
 CC properties. Reduced production of C14SR can increase the life-span of
 CC plants and produce plants having reduced and more compact proportions.
 CC Overproduction is useful for enhancing the production of medically or
 CC agriculturally useful steroid compounds. C14SR polypeptides are also
 CC useful for the development of enzyme inhibitors of the sterol
 CC biosynthetic pathway

XX SQ Sequence 1429 BP; 369 A; 269 C; 305 G; 481 T; 0 U; 5 Other;

Alignment Scores:

Pred. No.: 7,88e-158 Length: 1429
 Score: 1569.50 Matches: 294
 Percent Similarity: 86.36% Conservative: 29
 Best Local Similarity: 78.61% Mismatches: 42
 Query Match: 79.87% Indels: 9
 DB: 2 Gaps: 2

US-10-069-427-8 (1-369) x AA04237 (1-1429)

QY 1 MetMetGluSerHisValAspLeuGlyPheLeuLeuGlnAlaLeuThrProSerTrpAsn 20
 DB 81 TTAATGCTGCTAGATGGATCGGTGTCCTT-----CCATCATGGCAA 128
 QY 21 SerValProLeuLeuValGlyPhePheThrTyrLeuAlaValAlaGlySerIleLeuPro 40
 DB 129 TCGTTTATGCTGCTGTTTACTTCTGTTTACTTGGCCGTTGCCGGAATTTCTCCC 188
 QY 41 GlyLysLeuValProGlyValAlaLeuLeuAspGlyThrArgLeuHisTyrCysAsn 60
 DB 189 GGGAAAGTTATTCCGCGCGCTCTTTTATCAGATGGCTCTCAACTTCGTTACCGATGCAAT 248
 QY 61 GlyLeuSerLeuLeuLeuValAlaLeuLeuGlyIleGlyValAlaLysMetGlyPhe 80
 DB 249 GGTCTATTGGCAATAATTGTTGGTAGTATTTTGGGAATCTGTGCAAACTTGGCATT 308
 QY 81 ValSerProThrAlaIleSerAspArgGlyLeuGluLeuLeuSerThrThrPheAlaPhe 100
 DB 309 GTATCACCCTTCTGCTGGGATAGGACATTGAGTTACTCTCAGTACTTTTATTTC 368
 QY 101 SerPheLeuValThrLeuLeuLeuHisPheSerGlyCysLysSerClnSerLysGlySer 120
 DB 369 TGTGTTTGTGTGACATTAGCATTTGATGTTATGCGCGGAAGTTCTCTCGAATAAGGGTTCT 428
 QY 121 SerLeuLysProHisLeuSerGlyAsnLeuIleHisAspTrpTrpPheGlyIleGlnLeu 140
 DB 429 TCCTTAAGGCTCATCTCAGGAATCTTGACATGACTGTGGTGTTCGAATACAGCTG 488
 QY 141 AsnProClnPheMetGlyIleAspLeuLys-----AlaClyMetMetGly 155
 DB 489 AATCCTCAGTTTATGAGCATGATGATCAAGTTTCTTTGTGACGCCGGGATGATGGGA 548
 QY 156 TrpLeuLeuIleAsnLeuSerIleLeuMetLysSerIleGlnAspGlyThrLeuSerGln 175

DB 549 TGCGTGTCTATCAATCTCTCTATTCTGGCAAAAGTGTGCAGGATGTCCTTGAGTCAG 608
 QY 176 SerMetIleLeuTyrGlnLeuPheCysAlaLeuTyrIleLeuAspTyrPheValHisGlu 195
 DB 609 TCGATGATCTTACCAGATCTCTCTGCGTTATATATATATATATATATGAGTACTTGTTCATGAA 668
 QY 196 GluTyrMetThrSerThrTrpAspIleIleAlaGluArgLeuGlyPheMetLeuValPhe 215
 DB 669 GAATACATGACCTCTACGTGGACATAATTGCAGAGAGACTAGGCTTCATGCTAGTGT 728
 QY 216 GlyAspLeuValTrpIleProPheSerPheSerIleGlnGlyTrpTrpLeuLeuMetAsn 235
 DB 729 GGAGATCTCTGTGATCTCTCTTCACTTTAGCATTCAGGGCTGTGGCTTTTGCACAC 788
 QY 236 SerValGluLeuThrProAlaIleValAlaAsnCysPheValPheIleGlyTyr 255
 DB 789 AAGTAGAAGTAACAGTCTCTGCGATTGTAGTCAATTGCTTCTTCTGTAGGGTAC 848
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 DB 849 ATGTTTTTTCGAGAGCTAAACAACAACAACAATATCTTTAAGAAAGAACCCCAAAACACCA 908
 QY 276 IleTrpGlyLysProLysValIleGlyGlyLysLeuAlaSerGlyTyrTrpGly 295
 DB 909 ATATGGGCAAGCTCCAGTGGTAGTTGGTGGAAAGTTACTGGTTTCAGGCTATTGGGA 968
 QY 296 IleAlaArgHisCysAsnTyrLeuGlyAspLeuMetLeuAlaLeuSerPheSerLeuPro 315
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 QY 316 CysGlyIleSerSerProIleProTyrPheTyrProIleTyrLeuLeuLeuLeuLeu 335
 DB 1029 TGTGGATAAGTTCTCGGGTTCATATTTCTACCCGATATACCTTCTGATACTATTGATA 1088
 QY 336 TrpArgGluArgThrAspGluAlaArgCysAlaGluLysTyrArgGluIleTrpAlaGlu 355
 DB 1089 TGGAGAGACGAAGACAGACGAGGTTCCGATGTGCAGAGAAGTACAGAGATATGGGCAGAG 1148
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 DB 1149 TATCTTAGACTTGTCCCTCGAGAAATACITCTTTATGTTTAT 1190
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 AAC45795
 ID AAC45795 standard; DNA; 1110 BP.
 XX AAC45795;
 AC AAC45795;
 DT 18-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 47790.
 KW Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway; metabolic pathway;
 KW promoter; termination sequence; ss.
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 XX
 XX 06-SEP-2000.
 PD
 XX
 PF 25-FEB-2000; 2000EP-00301439.
 XX
 PR 25-FEB-1999; 99US-0121825P.
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PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 7e-158 Length: 1110
Score: 1568.50 Matches: 293
Percent Similarity: 86.99% Conservative: 28
Best Local Similarity: 79.40% Mismatches: 39
Query Match: 79.82% Indels: 9
DB: 3 Gaps: 2

US-10-069-427-8 (1-369) x AAC45795 (1-1110)

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DB 13 ATGGATCTCGGTGTTCTTCTT-----CCATCATTCGAAATCTGTTATGTGCTG 60
QY 26 ValGlyPhePheThrTrpLeuAlaValAlaGlySerIleLeuProGlyLysLeuValPro 45
DB 61 GTGTTTACTCTGTTACTTGGCCGTTGCCGGAATTTCTCCCGGGAAGATTATTCG 120
QY 46 GlyValAlaLeuLeuAspGlyThrArgLeuHisTyrCysCysAsnGlyLeuLeuSerLeu 65
DB 121 GCGGTCCTTTTATCAGATGGCTCTCAACTTCGTTACCGATGCAATGGTCTATTGGCACTA 180
QY 66 LeuLeuLeuValAlaLeuLeuGlyIleGlyAlaLysMetGlyPheValSerProThrAla 85
DB 181 ATATTCTTGATAGTATTTTGGGAATCTCTGCAAACTTGGCAATGTATCACCCTCTTG 240
QY 86 IleSerAspArgGlyLeuGluLeuLeuSerThrPheAlaPheSerPheLeuValThr 105
DB 241 GTTCGGATAGAGACTTGAATGTTACTCTCAGTACTTTTATTTCTGCTGTTGTGACA 300
QY 106 LeuIleLeuHisPheSerGlyCysLysSerGlnSerLysGlySerLeuLysProHis 125
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QY 126 LeuSerGlyAsnLeuIleHisAspTrpTrpPheGlyIleGlnLeuAsnProGlnPheMet 145
DB 361 GTCTCAGGAATCTTGTACATGACTGGTGTGTTGGAAATACAGTGAATCTCAGTTTATG 420
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QY 161 LeuSerIleLeuMetLysSerIleGlnAspGlyThrLeuSerGlnSerMetIleLeuVal 180
DB 481 CTCTCTATTCTGGCAAAAAGTGTGAGGATGGTTCCTTGAGTCAGTCGATGATTTCTTTAC 540

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QY 181 GlnLeuPheCysAlaLeuTyrIleLeuAspTyrPheValHisGluGluTyrMetThrSer 200
DB 541 CAGATCTTCGTGCGTATATATATATTTGGACTACTTTGTTTCATGAAGATACATGACCTCT 600
QY 201 ThrTrpAspIleIleAlaGluArgLeuGlyPheMetLeuValPheGlyAspLeuValTrp 220
DB 601 ACGTGGACATAATTCAGAGAGACTAGGCTTCATGCTAGTGTGTTGGAGATCTCTCTGG 660
QY 221 IleProPheSerPheSerIleGlnGlyTrpTrpLeuLeuMetAsnSerValGluLeuThr 240
DB 661 ATTCCTTTTACATTTTAGCATTCAGGCTGTGCTTTTGCACAACTAGACTAACA 720
QY 241 ProAlaAlaIleValAlaAsnCysPheValPheLeuIleGlyTyrMetValPheArgGly 260
DB 721 GTTCCTGGCATTTAGTCAATTCCTTCTTGTATAGGTACATGCTTTTTCGAGGA 780
QY 261 AlaAsnLysGlnLysHisValPheLysLysAsnProLysAlaProIleTrpGlyLysPro 280
DB 781 GCTAACAAACAAACATATCTTTAAGAAGAACCCAAACACCAATATGGGGCAGACCT 840
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QY 301 AsnTyrLeuGlyAspLeuMetLeuAlaLeuSerPheSerLeuProCysGlyLysSerSer 320
DB 901 AATTACCTTGGCAGTTGATGCTTGTCTCTCTCCTCAGTTTGCATGTGGAATAAGTTCT 960
QY 321 ProIleProTyrPheTyrProIleTyrLeuLeuIleLeuLeuIleTrpArgGluArgThr 340
DB 961 CCGTTCCATTTTCTACCGCATATACCTTCTGATACTATTGATATGGAGAGACGAAGA 1020
QY 341 AspGluAlaArgCysAlaGluLysTyrArgGluIleTrpAlaGluTyrArgLysLeuVal 360
DB 1021 GACGAGTTTCGATGTGCAGAGAACTACAAGAGATATGGCAGAGTATCTTACACTTGT 1080
QY 361 ProTrpArgIleLeuProTyrValTyr 369
DB 1081 CCCTGGAGATACTCTCTTATGTTTAT 1107

RESULT 5
AAC37623
ID AAC37623 standard; DNA; 1380 BP.
XX AAC37623;
AC AAC37623;
DT 17-OCT-2000 (first entry)
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 18063.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 18063.
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway; metabolic pathway;
XX promoter; termination sequence; ss.
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX 06-SEP-2000.
PD 25-FEB-2000; 2000EP-00301439.
PF 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 29-MAR-1999; 99US-0126264P.
PR 01-APR-1999; 99US-0126785P.
PR 06-APR-1999; 99US-0127462P.
PR 08-APR-1999; 99US-0128234P.
PR 16-APR-1999; 99US-0128714P.
PR 19-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.

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PR 21-APR-1999; 99US-0130449P.
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PR 11-MAY-1999; 99US-0134256P.
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PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
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PR 19-JUL-1999; 99US-0144335P.

PR 20-JUL-1999; 99US-0144352P.
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PR 09-AUG-1999; 99US-0147439P.
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PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
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PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
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PR 10-SEP-1999; 99US-0153070P.
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PR 04-OCT-1999; 99US-0157117P.
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QY 84 -----Thr-AlaIleSerAspArgGlyLeu 93
Db 3945 TTCTCACACTCATCCACTAGATGTTGGTAGGTGGGATAGAGACTTGAGTTA 4004
QY 94 LeuSerThrPheAlaPheSerPheLeu----- 103
Db 4005 CTCTAGCTACTTN-NATTTCTGTGTGGGGAAGATCAATCCCTAGTCCGGNGTC 4063
QY 103 ----- 103
Db 4064 TTGGATTTAGTNGTATTACCATCAGATTNGCTTTGGGTGTGTAATTGTAATCTCCAT 4123
QY 104 -----ValThrLeuIleLeuHisPheSerGlyCysIysSerGln 116
Db 4124 GATATCTCTTAATATTCTCAGGTGACATTAGCAATTGTATGTTACTGGCGAAGTCTCTCG 4183
QY 117 SerIysGlySerSerLeuIysProHisLeuSerGlyAsnLeuIleHisAspTrp----- 134
Db 4184 AATAAGGGTCTTCCCTAAGCTCATGCTCTCAGGAATCTTGTATACATCACTGTGTACTAA 4243
QY 134 ----- 134
Db 4244 CATAATACAAATTGTAGATCTGATCTTCTGTGTACACAAATGTTGTAAAGTTATAT 4303
QY 134 ----- 134
Db 4304 ATTTTGACTCTCTCAAGAGCAAACTAAGAAATATCTGGTACTATATAGAGTTTGAAGAAC 4363
QY 134 ----- 134
Db 4364 ACTGAATTGCAAGATGATTTCTATAGAACTTGTAGAGTGTGTAGTAATTTCTCCTAGA 4423
QY 134 ----- 134
Db 4424 ACGTTGTAGCTTCTCTTTTCTCTTTTAAACCGCAGTCACTTTAGCTTTTGGAACTTT 4483
QY 134 ----- 134
Db 4484 CTACTGAAACTAGAAAGTCTCTGTTTGTCTTCTCACTTATCTCTTCCAAACAACTGCTTCA 4543
QY 135 -----TrpPheGlyIleGlnLeuAsnProGln 143
Db 4544 ATTTTCTCATATGTTGTTTTCATGTAGTGGTGTGGAAATCACTGAACTCTCA 4603
QY 143 nPheMetGlyIleAspLeuIys----- 150
Db 4604 GTTATGAGCAATTGAATCTCAAGTAATCCATTTTCTGTTTCTTCTTATTTGTGAGCCA 4663
QY 150 ----- 150
Db 4664 AGGCTACATCATTTGCTTCACTTTGTTCCGTPACTCAATCGAGTGGCAGTTTAATAATGTAA 4723
QY 150 ----- 150
Db 4724 TCAGCAGTTATGATGTTATGATGAATGGAGTTATCTCTGTGTAGGTTTCTTTGT 4783
QY 151 -----AlaGlyMetMetGlyTrpLeuLeuIleAsnLeuSerIleLeuMetIysSerIleGln 169
Db 4784 CAGAGCCGGGATGATGGATGGCTGCTTATCAATCTCTCTATTTCTGCGAAAAAGTGTGCA 4843
QY 169 nAspGlyThrLeuSerGlnSerMetIleLeuTyrglnLeuPheCysAlaLeu----- 186
Db 4844 GGATGGTTCCTTGAGTCAGTCGATGAT-CTTTACCAGATCTCTGTCGGGTAAATTTGGT 4902
QY 186 ----- 186
Db 4903 TTTTACTTACAAATCTTGTCTTGAATCTGATCATCTGTGTTTGTGTAGTTTTCATTA 4962
QY 187 -----TyrIle-LeuAspTyrrPheValHisGluGluTyrrMetThrSerT 201
Db 4963 GTTTTATAATTGCAAGTTATATATATGATACATTGTTATGGAATATACATACCTCTTA 5022
QY 201 hr----- 201

Db 5023 CGTAAGTTTCATGCGGTGTTAAGGAACACATTTGTTCTTACCAAAAAATGACCATTTGTCAT 5082
QY 202 -----TrpAspIleIleAlaGluArgLeuGly 210
Db 5083 TATTACATCTACTTTTGATTTTACTCTTTTCAGGTGGGACATATTTCAGAGAGACTAGGC 5142
QY 211 PheMetLeuValPheGlyAspLeuValTrpIleProPheSerPheSerIle----- 227
Db 5143 TTCACTAGTAGTTTGGAGATCTCTCTGTGATCTCTTTTTCATCTTTTAGCATTCAGGCATGT 5202
QY 227 ----- 227
Db 5203 AACTGTGAGCTCGAACACACAAAGATATTAAATTTATCTTATTGACAGTATCTTCTTGGC 5262
QY 227 ----- 227
Db 5263 ATGTTACAGTTATCTCGGAAACAAATATTGTTCTAGAAATGCTTGATCACTCTGTGACTCA 5322
QY 228 -----GlnGlyTrpTrpLeuLeuMetAsnSerValGlnLeuThrPro 241
Db 5323 ATTGCTTCTCTCTGTGTACAGGGCTGGTGGCTTTTGCAACAACAAAGTAGAACATAAT 5382
QY 242 AlaAlaIleValAlaAsnCysPheValPheLeuIle-Gly----- 254
Db 5383 CTTGCGATTTGTAGTCAATTCCTTGTCTTCTTGTATAGGTAACTCTGTGAGACATGGGTT 5442
QY 255 -----TyrMe 256
Db 5443 ATTTTCCATTTTACATATCTACACTAAGAAACCCACTATTTCTTCTTGGCAGGTACAT 5502
QY 256 tValPheArgGlyAlaAsnLysGlnIysHisValPheLysLysAsnProIysAlaProI 276
Db 5503 GGTTTTTCGAGGAGCTAACCAACAAACATATCTTTAAGAAAGAACCCAAAAACCAAT 5562
QY 276 eTrpGlyLysProProLysValIleGlyLysLeuLeuAlaSerGlyTyrrP----- 294
Db 5563 ATGGGCAAGCTCCAGTGTGTAGTGTGGTGAAGTACTTGGTTTTCAGGCTATTGGTATGT 5622
QY 294 ----- 294
Db 5623 TATATTTATCTCTCTTGTGTTTCTTGTGTTTTCGCAATCTCTGTGTTTGTGTTGTCAT 5682
QY 294 ----- 294
Db 5683 CATCTGGGAATAAAGAGTTGAAAGTTCCGCAATGACACATTTCCGTAATCTTAGGTGCT 5742
QY 295 -----GlyIleAlaArgHisCysAsnTyrrLeuGlyAspLeuMetLe 308
Db 5743 GTTTTGTATATATGACAGGGGAATTTGCAAGGCACTGTAAATACCTTGGCAGCTTGATGT 5802
QY 308 uAlaLeuSerPheSerLeuProCysGlyIle----- 318
Db 5803 TGCTCTGCTCTTCAAGTTTGCATGTGGAATAAGTACTCCTCTGCTGTGAGTTCACCTAC 5862
QY 318 ----- 318
Db 5863 AGCTACCAAAATCATGTAGAACTAATACCAATATCAAAAGTTCGAAGTTGATTTGGCT 5922
QY 318 ----- 318
Db 5923 GACTTAAAGATATTGATCTCTAACCATCATGTGAAAGTCTAAAGCTTCAAGTTCAATTT 5982
QY 319 -----SerSerProIleProTyrrPh 325
Db 5983 CCCAAAGCTGTTTTATGATATTTCGTCTNGTGTATTCTCAGTTCTCCGGTTCATATTT 6042
QY 325 eTyrrProIleTyrrLeuLeuIleLeuLeuIleTrpArgGluArgThrAspGluAlaArgCy 345
Db 6043 CTACCCGATATACCTGCTGATACCTATTGATATGGAGAGAACGAGACGAGGTTCGATG 6102
QY 345 sAlaGluLysTyrrArgGluIleTrpAlaGluTyrrArgLysLeuValProTrpArgIleLe 365

Db 6103 TGCAGAGAGTACNAGAGAGATATGGCAGAGTATCTTAGACTTGTCCCTGGAGATACT 6162

Qy 365 uProTyValTyr 369

Db 6163 TCCTTAGTTTAT 6175

RESULT 7

ADD17001

ID ADD17001 standard; DNA; 625 BP.

XX AC

XX AC

XX DT

XX DE

XX DE

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

XX OS

XX OS

XX PN

XX PN

XX PD

XX PD

XX PF

XX PF

XX PR

XX PR

XX PA

XX PA

XX PI

XX PI

XX DR

XX DR

XX PT

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XX PT

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XX CC

XX CC

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XX CC

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XX CC

XX CC

Qy 166 LysSerIleGlnAspGlyThrLeuSerGlnSerMetIleLeuTyrGlnLeuPheCysAla 185
 Db 2 AAATGTAATCTAAAAACCAAACTGAGCAATCAATGAGGCTCTACACGCTATTTTGTGGG 61
 Qy 186 LeuTyrIleLeuAspTyrPheValHisGluGluTyrMetThrSerThrTrpAspIleIle 205
 Db 62 CTGTACATCCTTGATTTACTTCTCTGTGAAGAGTTTCATGACCTCCACATGGATATAATA 121
 Qy 206 AlaGluArgLeuGlyPheMetLeuValPheGlyAspLeuValTrpIleProPheSerPhe 225
 Db 122 GCAGAGAGGTTGGGCTTCATGCTGGTTTTTGGTATCTAGTCTTTATACCGTTCACCTTC 181
 Qy 226 SerIleGlnGlyTrpTrpLeuLeuMetAsnSerValGluLeuLeuThrProAlaIleVal 245
 Db 182 AGTATTACGGGTTGGTGGCTTTTTCAGTAACAAAGTGAACCTAACACAGCAGCAGTAATT 241
 Qy 246 AlaAsnCysPheValPheLeuIleGlyTyrMetValPheArgGlyAlaAsnLysGlnLys 265
 Db 242 GCCAATTGCTCGCTCTTCTTATTGGGTACTTGTGTTTCAGAGGTGCCAACAGCAGAGAG 301
 Qy 266 HisValPheLysLysAsnProLysAlaProIleTrpGlyLysProProLysValIleGly 285
 Db 302 CATATGTTTAAAAAGAAATCCCAAGGCACCCATATGGGTAAGCCTCCAAAAAGTTATTGGG 361
 Qy 286 GlyLysLeuLeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeuGlyAsp 305
 Db 362 GGGAGATTGCTCGCTCTTCTGCTATTGGGCAATTCGTCGACACTGTAATTACCTTGGAGAT 421
 Qy 306 LeuMetLeuAlaLeuSerPheSerLeuProCysGlyIleSerSerProIleProTyrPhe 325
 Db 422 TTGTTGCTGGCATTGTCATTAGTTTGCCTTGTGGGATAAGTTCCGGGTTCCATACCTTT 481
 Qy 326 TyrProIleTyrLeuLeuIleLeuIleLeuIleLeuIleLeuIleLeuIleLeuIleLeu 345
 Db 482 TACCCCATATATCTTCTTATTCTCTAATATGGAGGAGAGAGGATGAAGCTCGATGT 541
 Qy 346 AlaGluLysTyrArgGluIleTrpAlaGluTyrArgLysLeuValProTrpArgIleLeu 365
 Db 542 GCAGAGAGTACAAAGAGCTGTGGACAGATACCGTAAACTTGTCTTGGAGGATATAATA 601
 Qy 366 ProTyrValTyr 369
 Db 602 CCGTACGTTTAC 613

RESULT 8

AAF30674

ID AAF30674 standard; cDNA; 427 BP.

XX AC

XX AC

XX DT

XX DT

XX DE

XX DE

XX KW

XX KW

XX KW

XX KW

XX OS

XX OS

XX FH

XX FH

XX FT

XX FT

XX FT

XX FT

XX PN

XX PN

XX PD

XX PD

XX PF

XX PF

XX PR

XX PR

XX PA

XX PA

This invention relates to the identification and isolation of novel nucleic acid molecules that confer altered visual phenotypes in plants. Specifically, it refers to modifications of plant architecture and/or leaf surface features in plants, such as chlorotic, bleaching, etching, wet leaf, stunting, elongation and texture phenotypes, which are thought will be agronomic traits beneficial to the farmer. As such, these novel phenotypes can affect growth regulation i.e. useful for creating dwarf varieties, exhibit resistance to insects or heat stress, confer changes in pigment content such that plants have enhanced vitamin production or delayed senescence and also for example produce plants that control the production of ethylene. Furthermore, the present invention comprises generating transgenic plants, as well as reproducibly altering the visual phenotype of plant seeds, plant tissues and plant cells containing the polynucleotides described herein. This polynucleotide is a homologue of a DNA sequence that confers an altered visual phenotype when expressed in plants, the method of the invention.

SQ Sequence 625 BP; 165 A; 117 C; 149 G; 194 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.84e-94 Length: 625
 Score: 973.00 Matches: 176
 Percent Similarity: 92.16% Conservative: 12
 Best Local Similarity: 86.27% Mismatches: 16
 Query Match: 49.52% Indels: 0
 DB: 9 Gaps: 0

US-10-069-427-8 (1-369) x ADD17001 (1-625)

(DUPO) DU PONT DE NEMOURS & CO E I.

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XX Famodu OO, Kinney AJ;
PI WPI; 2001-266146/27.
DR P-PSDB; AAB20378.
DR Novel gene encoding sterol delta-14 reductase useful for transgenic plant
PT production with altered sterol delta-14 reductase.
XX Claim 7; Page 35; 45pp; English.
XX The present sequence is that of expressed sequence tag clone
CC src3c.pk009.ci, which includes a partial coding region for soybean sterol
CC delta-14 reductase (see AAB20378). The clone was isolated from a cDNA
CC library prepared from soybean 8-day-old root infected with cyst nematode,
CC following database homology searches. The predicted polypeptide shows
CC amino acid sequence homology to Arabidopsis thaliana sterol delta-14
CC reductase. The invention relates to isolated polynucleotides encoding
CC sterol delta-14 reductases and to transgenic plants comprising such
CC polynucleotides. It also relates to the construction of a chimeric gene
CC encoding all or a portion of the sterol delta-14 reductase, in sense or
CC antisense orientation, where expression of the chimeric gene results in
CC production of altered levels of the enzyme in a transformed host cell.
CC The availability of plant sterol delta-14 reductase genes will provide a
CC means of altering sterol production and/or composition of plants, to
CC identify compounds that may be useful as novel herbicides and fungicides,
CC and to identify mutants of these genes that are resistant to these
CC herbicides and will enable the production of herbicide-resistant crops
XX SQ Sequence 427 BP; 86 A; 106 C; 95 G; 139 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 4,21e-66 Length: 427
Score: 706.00 Matches: 136
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.27% Mismatches: 0
Query Match: 35.93% Indels: 0
DB: 4 Gaps: 0

US-10-069-427-8 (1-369) x AAF30674 (1-427)
QY 1 MetMetGluSerHisValAspLeuGlyPheLeuLeuGlnAlaLeuThrProSerTrpAsn 20
DB 4 ATGATGGAGTCACACGTGGATCTAGGTTTCTCTTCAAGCTCTCACTCCATCTTGGAAC 63
QY 21 SerValProLeuLeuValGlyPhePheThrThrLeuAlaValAlaGlySerIleLeuPro 40
DB 64 TCGTTCTCTTGTGTTGGGGTCTTCACTTACTTGGCCGTGGATCCATCTCCCT 123
QY 41 GlyLysLeuValProGlyValAlaLeuLeuAspGlyThrArgLeuHisTyrCysAsn 60
DB 124 GGAATACTTCTCTGGCGTTGCTACTCTCGATGGAACCTCGTACACATATTGCTGCAAT 183
QY 61 GlyLeuLeuSerLeuLeuLeuValAlaLeuLeuGlyIleGlyAlaLysMetGlyPhe 80
DB 184 GGTCTGCTCTCGTCTCTTCTTGTGGTGCATCTCTCGGATCGGTGCCAAGATGGGTTT 243
QY 81 ValSerProThrAlaIleSerAspArgGlyLeuGluLeuLeuSerThrThrPheAlaPhe 100
DB 244 GTGTCCTCCACTGCCATATACAAACAGAGACTTGAGCTGCTGCCACAACTTTGCTTTC 303
QY 101 SerPheLeuValThrLeuLeuLeuHisPheSerGlyCysLysSerClnSerLysGlySer 120
DB 304 AGTTTCTTGTAAACCTGTATTCATTTTTCGGGTGCAAGTCACAAAGTAAAGNTCA 363
QY 121 SerLeuLysProHisLeuSerGlyAsnLeuIleHisAspTrpPheGly 137
DB 364 TCACTAAAGCCTCATCTCAGTGGGAACCTGATACACAGATTGTTGGTGGT 414

RESULT 9
ABK35567
ID ABK35567 standard; DNA; 3714 BP.
XX

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AC ABK35567;
XX 06-MAY-2002 (first entry)
XX Gene LBR differentially expressed in breast cancer tissue.
XX Human; diagnosis of breast cancer; endometrial cancer; breast tumour;
XX MAI; mitotic activity index; cytostatic; gene; ds.
XX Homo sapiens.
XX WO200210436-A2.
XX 07-FEB-2002.
XX 27-JUL-2001; 2001WO-US023642.
XX 28-JUL-2000; 2000US-0222093P.
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
XX (BRAK/) BRAK J.
XX Baak J, Mutter GL;
XX WPI; 2002-180084/23.
XX P-PSDB; AAU84347.
XX Diagnosing breast cancer comprises determining expression of nucleic acid
XX molecules or expression products that are differentially expressed in
XX normal and malignant tissue.
XX Claim 1; Page 94-96; 219pp; English.
XX The present invention relates to a method for diagnosing breast cancer in
XX a subject suspected of having endometrial cancer. The method comprises
XX determining the expression of a set of human genes or expression products
XX in an endometrial sample suspected of being cancerous. The human genes of
XX the invention are differentially expressed in breast tumours
XX characterised as high or low MAI (mitotic activity index). These sets of
XX genes can be used to discriminate between high and low MAI breast
XX tumours. The invention also provides DNA and protein microarrays for
XX analysing the expression of the human genes and their protein products.
XX The methods and arrays are useful for the diagnosis and prognosis of
XX endometrial cancer, selecting and monitoring treatment regimes, and
XX identification of compounds useful for the treatment of endometrial
XX cancer. ABK35531-ABK35581 represent the human genes of the invention that
XX are differentially expressed in breast cancer tissue.
XX SQ Sequence 3714 BP; 1046 A; 644 C; 759 G; 1265 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.31e-56 Length: 3714
Score: 630.00 Matches: 145
Percent Similarity: 55.70% Conservative: 65
Best Local Similarity: 38.46% Mismatches: 127
Query Match: 32.06% Indels: 40
DB: 6 Gaps: 11

US-10-069-427-8 (1-369) x ABK35567 (1-3714)
QY 8 LeuGlyPheLeuLeuGlnAlaLeuThrProSerTrpAsnSerValProLeuLeuValGly 27
DB 865 CTGGGTTTGTGATTCAGTCTG-----CTACTGCCAATTGGAAGGTTGTAGAGGA 898
QY 28 PhePheThrTyrLeuAlaValAlaGlySerIleLeuPro---GlyLysLeuValProGly 46
DB 889 TTCTAC-----CTACTGCCAATTGGAAGGTTGTAGAGGA 924
QY 47 ValAlaLeuLeuAspGlyThrArgLeuHisTyrCysAsnGlyLeuLeuSerLeuLeu 66
DB 925 ACGCCTCTTATTGATGGAAGAGACTCAAGTATAGATTAATGATCTCTATCTTTATC 984
QY 67 LeuLeuValAlaLeuLeuGlyIleGlyAlaLysMetGlyPheValSerProThrAlaIle 86

```

Db 985 CTGACATCTGCAGTCATCGAATCTCTCTCCAGGC---GTACAGTTTCATTACG 1041
QY 87 SerAspArgGlyLeuGluLeuSerThrPheAlaPheSerPheLeuValThrLeu 106
Db 1042 TACAGTCATTTCTTCAGTTTGGCACTTGGCCGACCTGTTTGTGTGTCTGTAGTGG 1101
QY 107 IleLeuHisPheSerGlyCysLysSerSerGlySerLeuLeuProHisLeu 126
Db 1102 TATCTCTACATCGCTCTTTGAAAGCGCCCG---AATGACCTGTGCGCTGCCAG 1155
QY 127 SerGlyAsnLeuLeuHisAspTrpPheGlyIleGlnLeuAsnProGlnPheMetGly 146
Db 1156 TCTGGAAATCTCTCATGATTTCTTCATGCGCGGTAATTAACCTCGAATGGTACT 1215
QY 147 IleAspLeuLys-----AlaGlyMetMetGlyTrpLeuLeuLeuAsn 160
Db 1216 TTTGATCTCAATACITTTTGTAATTGCGCCCGGATTCGATGGGTGGTATTAAAC 1275
QY 161 LeuSerIleLeuMet-----LysSerIleGlnAspGlyThrLeu---SerGlnSerMet 177
Db 1276 TTGCTGATGCTTTTGGCTGAAATGAAATACAGGACCGCGCTGTTCCATCCTTGGCCATG 1335
QY 178 IleLeuTyrGlnLeuPheCysAlaLeuTyrIleLeuAspTyrPheValHisGluGluTyr 197
Db 1336 ATTTAGTTAATAGTTTCAGCTTCTTAIGTGTGATGCTCTCTCGAATGAGGAAGG 1395
QY 198 MetThrSerThrTrpAspIleAlaGluArgLeuGlyPheMetLeuValPheGlyAsp 217
Db 1396 TTGTCGACGACCATGACATCATCCAGATGATTTGGATTTCATGCTGCTTTTGAGAC 1455
QY 218 LeuValTrpIleProPheSerPheSerIleGlnGlyTrpTrpLeuLeuMet-----Asn 235
Db 1456 TTGCTGCTGCTTTTACAGCTTCTTACAGCTTCCAGCGCTTTATTTAGTACGTCATCAAT 1515
QY 236 SerValGluLeuThrProAlaIleValAlaAsnCysPheValPheLeuIleGlyTyr 255
Db 1516 GAAGTGTCTTGGCAATGCTCTCTAAT-----ATTGTTCTGAACTTTGTGTTAT 1569
QY 256 MetValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAsnProLysAlaPro 275
Db 1570 GTAATCTCCGAGGTGCAAAATCTCAGAAAAATGCAATCCGAAAAATCCCAAGTATCCA 1629
QY 276 IleTrpGlyLysProLysVal-----IleGlyGlyLysLeuLeuAlaSerGly 292
Db 1630 AGCTTGCACTTAAACCACTCATCTCAAGTGGAATAATCTTAGTTCTGGA 1689
QY 293 TyrTrpGlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuMetLeuAlaLeuSerPhe 312
Db 1690 TGTGGGGCTTTGTTCCGCCACCAATTAATCTGGGTGATCTCATGCGCTTGGCGTG 1749
QY 313 SerLeuProCysGlyIleSerProIleProTyrPheTyrProIleTyrLeuLeuLeu 332
Db 1750 TCCCTCCCAAGTGGTTTAAACACATCTGCGCTTATTTCTCATATTTATTTACCATG 1809
QY 333 LeuLeuIleTrpArgGluArgThrAspGluAlaArgCysAlaGluLysTyrArgGluIle 352
Db 1810 TTGCTTGTCCCGAGAGCTCGTGAGGAGTACCAGTCTGTAAGAGAAATACGCGGTGCT 1869
QY 353 TrpAlaGluTyrArgLysLeuValProTrpArgIleLeuProTyrValTyr 369
Db 1870 TGGGAAAGTACTGTCAGCGGTGCGCTTACCGCTATATTATTTCCATCATCTAC 1920

RESULT 10

ID ABK83864 standard; cDNA; 3714 BP.

XX AC ABK83864;

XX DT 14-AUG-2002 (first entry)

XX DE Human cDNA differentially expressed in granulocytic cells #435.

XX

KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX Homo sapiens.
OS WO200228999-A2.
PN 11-APR-2002.
PD 03-OCT-2001; 2001WO-US030821.
PF 03-OCT-2000; 2000US-0237189P.
PR (GENE-) GENE LOGIC INC.
PA Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
PI WPI; 2002-435328/46.
PS Detecting granulocyte activation by detecting differential expression of
PT genes associated with granulocyte activation, which serves as diagnostic
PT markers that is useful for monitoring disease states and drug toxicity.
XX Claim 1; SEQ ID NO 435; 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GCA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in an electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 3714 BP; 1046 A; 644 C; 759 G; 1265 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,31e-56 Length: 3714
Score: 630.00 Matches: 145
Percent Similarity: 55.70% Conservative: 65

Best Local Similarity: 38.46%		Mismatches: 127
Query Match: 32.08%		Indels: 40
DB: 6		Gaps: 11
US-10-069-427-8 (1-369) x ABK83864 (1-3714)		
QY	8 LeuGlyPheLeuLeuGluAlaLeuThrProSerTrpAsnSerValProLeuLeuValGly 27	
DB	865 CTGTGGTTTGTGATCAAGTCCTG-----888	
QY	28 PhePheThrTyLeuAlaValAlaGlySerIleLeuPro---GlyLysLeuValProGly 46	
DB	889 TTCTAC-----CTACTGCCAAATTGGAAGGTTGTAGAAGGA 924	
QY	47 ValAlaLeuLeuAspGlyThrArgLeuHisTyCysAsnGlyLeuLeuSerLeuLeu 66	
DB	925 AGCCCTCTATTATGATGGAAGAGACTCAAGTATAGATTAAATGGATTCTATCCCTTTATC 984	
QY	67 LeuLeuValAlaLeuLeuGlyIleGlyAlaLysMetGlyPheValSerProThrAlaIle 86	
DB	985 CTGACATCTGCAGTCATCGGAACATCTCTCTCCAGGCG---GTACAGTTTCATTACGTG 1041	
QY	87 SerAspArgGlyLeuLeuLeuSerThrThrPheAlaPheSerPheLeuValThrLeu 106	
DB	1042 TACAGTCATTTCTTCAGTTTCACATCTGCGGCCACTGTTTGTGTGCTCTGAGTGTG 1101	
QY	107 IleLeuHisPheSerGlyCysLysSerGlnSerLysGlySerSerLeuLysProHisLeu 126	
DB	1102 TATCTCTACATCGGCTTTTGAAGCGCCCG-----AATGACCTGTGCGCTGCCAGC 1155	
QY	127 SerGlyAsnLeuLeuHisAspTrpTrpPheGlyIleGlnLeuAsnProGlnPheMetGly 146	
DB	1156 TCTGGAATGCTGCTCTATGATTTCTTCATTGCGCGCGTGAATTAACCCCTCGAATTGGTACT 1215	
QY	147 IleAspLeuLys-----AlaGlyMetMetGlyTrpLeuLeuIleAsn 160	
DB	1216 TTGTATCTCAATATCTTTTGTGAATTCGCCCGCGATGATGGATGGTGGTTATTATAC 1275	
QY	161 LeuSerIleLeuMet-----LysSerIleGlnAspGlyThrLeu---SerGlnSerMet 177	
DB	1276 TTGGTGATGCTTTTGGCTGAATGAAATACAGGACCGCGCTGTCCTCCATCTCTGGCCATG 1335	
QY	178 IleLeuTyTrpLeuPheCysAlaLeuTyTrpIleLeuAspTyTrpPheValHisGluGluTy 197	
DB	1336 ATTTTATGTTAAATGTTTCCAGCTTCTATGTTGGTGGATGCTCTCTGGATGAGGAACG 1395	
QY	198 MetThrSerThrTrpAspIleIleAlaGluA-gLeuGlyPheMetLeuValPheGlyAsp 217	
DB	1396 TTGTTGACGACCATGACATCATCCAGCATGATTTGGATTCTGCTGCTTTGGAGAC 1455	
QY	218 LeuValTrpIleProPheSerPheSerIleGlnGlyTrpTrpLeuLeuMet-----Asn 235	
DB	1456 TTGGTGTGGGTTCCCTTTTATTTACAGCTTCCAGCGCTTTATTTAGTCAGTCATCCAAAT 1515	
QY	236 SerValGluLeuThrProAlaAlaIleValAlaAsnCysPheValPheLeuIleGlyTy 255	
DB	1516 GAAGTGTCTGGCCATGCTTCTTAAT-----ATTGTTCTGAACCTTTGTGTTAT 1569	
QY	256 MetValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAsnProLysAlaPro 275	
DB	1570 GTAATCTTCGAGGTGCAAAATCTCAGAAAAATGCAATTCGGAATAATCCAGTATCCA 1629	
QY	276 IleTrpGlyLysProProLysVal-----IleGlyGlyLysLeuAlaLeuSerGly 292	
DB	1630 AACCTTGCACATTTAAACCATTCTACTTCAAGTGGAAAAAATCTTAGTTCTGGA 1689	
QY	293 TyTrpGlyIleAlaAlaArgHisCysAsnTyTrpLeuGlyAspLeuMetLeuAlaLeuSerPhe 312	
DB	1690 TGGTGGGCTTTGTCGCCACCCCAATTAATTTGGGTGATCTCATCATGCGCTTGGCGTGG 1749	
QY	313 SerLeuProCysGlyLysSerProIleProTyPheTyTrpPheTyTrpLeuLeuLeu 332	
DB	1750 TCCCTCCCATGTGGTTTAAACCAACATTCGCTTATTTCTACATTAATTTATTTCCACATG 1809	

QY

333 LeuLeuIleTrpArgGluArgThrAspGluAlaArgCysAlaGluLysTyArgGluIle 352

DB

1810 TTGCTTGTCCACGAGAGCTCGTGACGAGTACCACCTGTAAAGAAGAAATACGCGGTGGCT 1869

QY

353 TrpAlaGluTyArgLysLeuValProTrpArgIleLeuProTyTrpValTy 369

DB

1870 TGGGAAAGTACTGTGAGCGTGTGCCCTATATATTTCCATCATCTTAC 1920

RESULT 11

AAF30676

ID

AAF30676 standard; cDNA; 667 BP.

XX

AAF30676;

AC

11-JUN-2001 (first entry)

DT

Soybean sterol delta-14 reductase clone src3c.pk009.cl.fis.

XX

Soybean; sterol delta-14 reductase; transgenic plant; herbicide;

XX

fungicide; ss.

XX

Glycine max.

OS

Key

Location/Qualifiers

XX

1. .423

FT

CDS

FT

/tag= a

FT

/partial

PN

W0200123539-A2.

XX

05-APR-2001.

XX

27-SEP-2000; 2000WO-US026442.

XX

30-SEP-1999; 99US-0156820P.

XX

(DUPO) DU PONT DE NEMOURS & CO E I.

XX

Famodu OO, Kinney AJ;

XX

WPI; 2001-266146/27.

XX

P-PSDB; AAB20380.

DR

Novel gene encoding sterol delta-14 reductase useful for transgenic plant

PT

production with altered sterol delta-14 reductase.

XX

Claim 7; Page 38; 45pp; English.

CC

The present sequence is that of the full insert sequence of clone

CC

src3c.pk009.cl, which includes a partial coding region for soybean sterol

CC

delta-14 reductase (see AAB20380). The clone was isolated from a cDNA

CC

library prepared from soybean 8-day-old root infected with cyst nematode,

CC

following database homology searches. The predicted polypeptide shows

CC

amino acid sequence homology to Arabidopsis thaliana and Arabobolus

CC

immus sterol delta-14 reductases. The invention relates to isolated

CC

polynucleotides encoding sterol delta-14 reductases and to transgenic

CC

plants comprising such polynucleotides. It also relates to the

CC

construction of a chimeric gene encoding all or a portion of the sterol

CC

delta-14 reductase, in sense or antisense orientation, where expression

CC

of the chimeric gene results in production of altered levels of the

CC

enzyme in a transformed host cell. The availability of plant sterol delta

CC

-14 reductase genes will provide a means of altering sterol production

CC

and/or composition of plants, to identify compounds that may be useful as

CC

novel herbicides and fungicides, and to identify mutants of these genes

CC

that are resistant to these herbicides and will enable the production of

CC

herbicide-resistant crops

XX

Sequence 667 BP; 204 A; 144 C; 161 G; 158 T; 0 U; 0 Other;

Alignment Scores:	1.02e-56	Length:	667
Pred. No.:	621.00	Matches:	111
Score:			

Db 715 AGTTGTTGCATTATACAGTACCATTAATTTGGGCTACGTAACAGACTCAATGATTGTTGTA 774
Qy 181 GlnLeuPheCysAlaLeuTyrIleLeuAspTyrPheValHisGluGluTyrMetThrSer 200
Db 775 AACTTACTTCAAGCATCTTACATATTCGATGGGTATTGACGAAGAAGGTTGTTGACG 834
Qy 201 ThrTrpAspIleAlaGluArgLeuGlyPheMetLeuValPheGlyAspLeuValTrp 220
Db 835 ATGATTGACATTAACCCAGCATGATTGTTGTTTATGCTTAAGCTTTGGTGACTTCGCTGG 894
Qy 221 IleProPheSerPheSerIleGlnGlyTrpTrpLeuMetAsnSerValGluLeuThr 240
Db 895 GTTCTTGACATTAATCTTACCAAGCAAGATATTGAGCATTAAGGCAATGAAGTCAAC 954
Qy 241 ProAlaAlaIleValAlaAsnCysPheValPheLeu-----IleGlyTyrMetValPhe 258
Db 955 TTAGGATGGACATTAAGTTTGTGATCGTTGGATTACAGGCATTAGGGTTTACATCTTC 1014
Qy 259 ArgGlyAlaAsnLysGlnLysHisValPheLysLysAsnProLysAlaProIleTrpGly 278
Db 1015 CGCTCAGCAATTAACCAAAAATCAGATTTTAGACAA-----GGT 1053
Qy 279 LysProProLysVal-----IleGlyGlyLysLeuLeuAlaSerGly 292
Db 1054 AGTTGCCCATTAATAAAGAGCATCCAAACTAAAGCTGGCTCAAAATTTGTTGGGAAGGC 1113
Qy 293 TyrTrpGlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuMetLeuAlaLeuSerPhe 312
Db 1114 TGTGGGGCTGTCTCAACACATTAATATTATTTGGGTGACTGTTGATTGATTGATTCTTGG 1173
Qy 313 SerLeuProCysGlyIleSerProIleProTyrPheTyrProIleTrpLeuLeuIle 332
Db 1174 TGTTCCTACTGCTTTCACACCCCATGACCTACTTTTACGTTATTACTTTGCTTCC 1233
Qy 333 LeuLeuIleTrpArgGluArgThrAspGluAlaArgCysAlaGluLysTyrArgGluIle 352
Db 1234 TTGCTAATCCATCGTCAAGTAAGAGACGAAATGAAAGTGACAGACAAATAACGGCAGGAT 1293
Qy 353 TrpAlaGluTyrArgLysLeuValProTrpArgIleLeuProTyrValTyr 369
Db 1294 TGGAAGAAGTACGAAAGCTAGTTCCTTATAAATAATTCCTTAATGATAT 1344

RESULT 13
AAQ89202
ID AAQ89202 standard; DNA; 2528 BP.
AC AAQ89202;
XX
DT 25-MAR-2003 (revised)
DT 23-SEP-1995 (first entry)
XX
DE Sterol-delta-14-reductase DNA.
XX
KW Sterol-delta-14-reductase; inhibitor; fungicide; morpholine; pML100; ds.
XX
OS Saccharomyces cerevisiae.
XX
FH Key Location/Qualifiers
FT 419..1735
FT CDS /*tag= a
XX
XX EP644268-A2.
XX
XX 22-MAR-1995.
XX
XX 29-JUL-1994; 94EP-00111839.
XX
XX 16-AUG-1993; 93US-00107348.
XX
XX (AMCY) AMERICAN CYANAMID CO.
XX
XX Lai MHK, Kirsch DR, Bard M;
XX

DR WPI; 1995-116992/16.
DR P-PSDB; AAR1934.
PT Screening method for sterol delta 14 reductase inhibitors - pref.
PT comprises binary assay using Neurospora crassa and Saccharomyces
cerevisiae.
XX
XX Disclosure; Page 17; 25pp; English.
XX
CC The S. cerevisiae sterol-delta-14-reductase gene was cloned by selecting
CC strains carrying sequences on a 2-mu vector for resistance to
CC fenpropimorph. Plasmid pML100 was isolated and shown to carry the
CC structural gene based upon the phenotype of gene disruption strains. The
CC DNA sequence of the 2.5 Sphi/XbaI fragment of pML100 is given in AAQ89202
CC and the encoded 50.5 kDa protein in AAR71934. Over-expression of the DNA
CC in yeast allows assay of inhibitor activity. (Updated on 25-MAR-2003 to
CC correct FN field.)
XX
SQ Sequence 2528 BP; 700 A; 469 C; 507 G; 852 T; 0 U; 0 Other;
Alignment Scores: 5.17e-48 Length: 2528
Pred. No.: 547.50 Matches: 133
Score: 53.87% Conservative: 76
Percent Similarity: 34.28% Mismatches: 136
Best Local Similarity: 27.86% Indels: 43
Query Match: 2 Gaps: 11
DB:
US-10-069-427-8 (1-369) x AAQ89202 (1-2528)
Qy 19 TrpAsnSerVal---ProLeu-----LeuValGly----- 27
Db 587 TGGAAACGGTATCAAGCCATTGCGCTACTATCTCGGCAATCGTGAATATGAGACTGTCTAT 646
Qy 28 -----PhePheThrTyrLeuAlaValAlaGlySerIleLeuProGlyLysLeuValPro 45
Db 647 TGCCTGGTATGGAAATACATCGGCGATTTCGAGCTCATTTTACCGGCGAGATCATGAAG 706
Qy 46 GlyValAlaLeuLeuAspGlyThrArgLeuHisTyrCysCysAsnGlyLeuLeuSerLeu 65
Db 707 GGTGTTTCAAGGATGGTTCGAAGCTTTCGTATAAGATCAATGGAATTCGATGTCT 766
Qy 66 LeuLeuValAlaLeuLeuGlyIleGlyAlaLys----- 77
Db 767 ACAACTTGGTCTTAGTTTGGCTATCAGATGGAATTCGATCGACATTCGCTGAA 826
Qy 78 MetGlyPheValSerProThrAlaIleSerAspArgGlyLeuGluLeuSerThrThr 97
Db 827 TTGCAATATCTGATGAAATACAGTTAGT-----TTATGCATAATATCTATTTTG 877
Qy 98 PheAlaPheSerPheLeuValThr-----LeuLeuLeu 108
Db 878 TTTTCGTGTC---TTTTTGGCGAGCTACTGCTATGTGCCAGCTTACCATTCATCTTC 934
Qy 109 HisPheSerGlyCysLysSerGlnSerLysGlySerSerLeuLysProHisLeuSerGly 128
Db 935 AAGAAATGTTAATGCGCAAGGAAAGATCTTAGCACTAGGTGGAAT---TCAGGA 991
Qy 129 AsnLeuIleHisAspTrpTrpPheGlyIleGlnLeuAsnProGlnPheMetGlyIleAsp 148
Db 992 AACATCATTTACGATTGGTTTATTGGTAGAGAACTGAACCTCGTCTCGGCCCATAGAT 1051
Qy 149 LeuLys-----AlaGlyMetMetGlyTrpLeuLeuLeuLeuSer 162
Db 1052 ATCAAGATGTTTTCAGAGTTGAGACCGGATGTTGTTATGTTACTGATCATCTTCC 1111
Qy 163 IleLeuMetLysSer---IleGlnAspGlyThrLeuSerGlnSerMetIleLeuTyrGln 181
Db 1112 TGTCTGCATCACCATTACCTGAAGACTGGTAAATCAACATGATCGTTCCTGGTGAAT 1171
Qy 182 LeuPheCysAlaLeuTyrIleLeuAspTyrPheValHisGluGluTyrMetThrSerThr 201
Db 1172 TTCTCGCAAGGATTTTACATTTTCGATGGAGTACTAAACGAGGAAGGTGATTAAACCATG 1231

QY 202 TrpAspIleLeuAlaGluArgLeuGlyPheMetLeuValPheGlyAspLeuValTrpIle 221
 Db 1232 ATGGATATCACTACAGATGGGTTTGGTTTCATGCTAGCGTTTGGTCACTTAAGTTAGTT 1291
 QY 222 ProPheSerPheSerIleGlnGlyTrpTrpLeuLeuMetAsnSerValGluLeuThrPro 241
 Db 1292 CCATTCACCTACTCATTAAGCCGCTTACTTGGTGTTCCTCGGAAATGGGATGG 1351
 QY 242 AlaAlaIleValAlaAsnCysPheValPheLeuIleGlyTyrMetValPheArgGlyAla 261
 Db 1352 GTGAAAGTTGCGGTATATTAGCCATAATGTTTGGGTTTCCACATCTTCCACTCGGCA 1411
 QY 262 AsnLysGlnLysHisValPheLysAsnProLysAlaProIleTrpGlyLysProPro 291
 Db 1412 AATAGCAAAATCTGAGTTAGACAAGGTAAATTAGAAAATCTAAAAAGTATTTCAGACA 1471
 QY 282 LysValIleGlyLysLysLeuLeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsn 301
 Db 1472 AAG--CGTGTACAAAGTTATTATGACGGGTGGGTAAATCACAGCATATCAAT 1528
 QY 302 TyrLeuGlyAspLeuMetLeuAlaLeuSerPheSerLeuProCysGlyIleSerSerPro 321
 Db 1529 TACTTTGGCGATTGGTGATTATTAAGTTGGTTTGGCCACCTGGTTCCAAACTCC 1588
 QY 322 IleProTyrPheTyrProIleTyrLeuLeuIleLeuLeuIleTrpArgGluArgThrAsp 341
 Db 1589 TTGACATATTACTACTCGTTGTTACTTCGCCACCTGTTTATTACACCTCAACACCTGAT 1648
 QY 342 GluAlaArgCysAlaGluLysTyrArgGluIleTrpAlaGluTyrArgLysLeuValPro 361
 Db 1649 GAGCACAAGTGGCGCTGAAATATGGCGAAATTTGGGAGAAATACGAAAGAAAGTTCT 1708
 QY 362 TrpArgIleLeuProTyrValTyr 369
 Db 1709 TACAGATCATTCATTAAGTTTAT 1732

RESULT 14
 AAT32142
 ID AAT32142 standard; DNA; 2528 BP.
 XX 20-SEP-1996 (first entry)
 XX Saccharomyces cerevisiae sterol delta-14 reductase gene.
 XX Sterol; delta-14; reductase; ergosterol; biosynthetic pathway;
 KW 2mu-based vector; resistance; morpholine; fungicide; fenpropimorph;
 KW screen; identification; biosynthesis; inhibition; agriculture; medicine;
 KW veterinary; application; ds.
 XX Saccharomyces cerevisiae.
 OS
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 419..1735
 FT /*tag= a
 XX
 XX US5512472-A.
 XX
 XX 30-APR-1996.
 XX
 XX 11-MAY-1995; 95US-00439131.
 XX
 XX 16-AUG-1993; 93US-00107347.
 XX
 XX (AMCY) AMERICAN CYANAMID CO.
 XX
 XX Bard M, Lai MHK, Kirsch DR;
 XX WPI; 1996-229870/23.
 DR P-PSDB; AAW01975.

XX S.cerevisiae sterol delta14 reductase gene - from the ergosterol
 PT biosynthesis pathway, is used to screen for sterol biosynthesis
 PT inhibitors for use as potential fungicides.
 XX
 PS Claim 3; Col 13-18; 20pp; English.
 XX
 CC The present sequence encodes the S. cerevisiae sterol delta-14 reductase,
 CC a component of the ergosterol biosynthetic pathway. The sterol delta-14
 CC reductase gene, which was isolated by selecting strains carrying
 CC sequences on a 2mu-based vector for resistance to a morpholine fungicide,
 CC e.g. fenpropimorph, or the enzyme can be used in screening tests for the
 CC identification of sterol biosynthesis inhibitors. The inhibitors are
 CC potential fungicides, which may be useful in a wide variety of
 CC agricultural, medical and veterinary applications. (Updated on 25-MAR-
 CC 2003 to correct PF field.)
 XX
 SQ Sequence 2528 BP; 700 A; 469 C; 507 G; 852 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 5,17e-48 Length: 2528
 Score: 547.50 Matches: 133
 Percent Similarity: 53.87% Conservative: 76
 Best Local Similarity: 34.28% Mismatches: 136
 Query Match: 27.86% Indels: 43
 DB: 2 Gaps: 11
 US-10-069-427-8 (1-369) x AAT32142 (1-2528)
 QY 19 TrpAsnSerVal---ProLeu-----LeuValGly----- 27
 Db 587 TGGACGGTATCAAGCCATTCGGCTACTATCTGGGCAATCGTAATTATGACTGTCTAT 646
 QY 28 -----PhePheThrTyrLeuAlaValAlaGlySerIleLeuProGlyLysLeuValPro 45
 Db 647 TGCCTGTGTTATGAATATCTGGCAGTTTGGACGTCATTTACCGGGCAGAGTCAAG 706
 QY 46 GlyValAlaLeuLeuAspGlyThrArgLeuHisTyrCysCysAsnGlyLeuLeuSerLeu 65
 Db 707 GGTGTTTCAGTTAAGGATGGTTGGAAGCTTTCGTATATAGATCAATGGAAATGCCATGTCT 766
 QY 66 LeuLeuLeuValAlaLeuLeuGlyIleGlyAlaLys----- 77
 Db 767 ACAACTTTGGTCTTAGTTTGGCTATCAGATGGAATTCAGTATGACAAATTGGCTGAA 826
 QY 78 MetGlyPheValSerProThrAlaIleSerAspArgGlyLeuGluLeuSerThrThr 97
 Db 827 TTGCAATATCTGTATGAAATCACGTTAGT-----TTATGCATAATATCATCTTTTG 877
 QY 98 PheAlaPheSerPheLeuValThr-----LeuIleLeu 108
 Db 878 TTTTCGTTTCTTTTGGCGACGCTACTGCTATGTTGCCAGCTTCATACCATTCATCTTC 934
 QY 109 HisPheSerGlyCysLysSerGlnSerLysSerGlySerSerLeuLysProHisLeuSerGly 128
 Db 935 AAGAAAAATGTTAATGCGCAAAAGGAAAGATCTTAGCCTAGGTGGAAAT---TCAGGA 991
 QY 129 AsnLeuIleHisAspTrpTrpPheGlyIleGlnLeuAsnProGlnPheMetGlyIleAsp 148
 Db 992 AACATCATTTACGATTGGTTTATGTTAGAGACTGAACCTCTCTCGGGCCCATTAGAT 1051
 QY 149 LeuLys-----AlaGlyMetMetGlyTrpLeuLeuIleAsnLeuSer 162
 Db 1052 ATCAAGATGTTTTCAGAGTTGAGACCGCGCATGTTGTTATGTTACTGATCAATCTTTCC 1111
 QY 163 IleLeuMetLysSer---IleGlnAspGlyThrLeuSerGlnSerMetIleLeuTyrGln 181
 Db 1112 TGCTTGATCACCATTCACCTGGAAGACTGGTAAATCAACGATGCATTCGTTCTTGGTAAAT 1171
 QY 182 LeuPheCysAlaLeuTyrIleLeuAspTyrPheValHisGluGluTyrMetThrThr 201
 Db 1172 TTCTCGCAAGGATTTTACATTTTCGATGGAGTAGTACTAAACGAGGAAGGTGATTAAACCATG 1231

QY 202 TrpAspIleAlaGluArgLeuGlyPheMetLeuValPheGlyAspLeuValTrpIle 221
 Db 1232 ATGGATATCACTACAGATGGTTGGTTTCATGCTAGCGTTTGGTCACTTAAGTTAGTT 1291

QY 222 ProPheSerPheSerIleGlnGlyTrpTrpLeuMetAsnSerValGluLeuThrPro 241
 Db 1292 CCATTCACTACTACTACAGCGCTTACTTGAGTGTTTCCCTGTGGAATTGGGATGG 1351

QY 242 AlaAlaIleValAlaAsnCysPheValPheLeuIleGlyTrpMetValPheArgGlyAla 261
 Db 1352 GTCAAGTTGTCGGTATATAGCCATAAGTTTGGGTTTCCACATCTTCCACCTCGCA 1411

QY 262 AsnLysGlnLysHisValPheLysLysAsnProLysAlaProIleTrpGlyLysPro 281
 Db 1412 AATAAGCAAAATCTGAGTTTAGCAAGGTAATAATAGAAAAATCTAAAAAGTATTACAGACA 1471

QY 282 LysValIleGlyLysLeuAlaSerGlyTrpGlyIleAlaArgHisCysAsn 301
 Db 1472 AAG---CGTGGTACAAAGTTTATGTGACGGGTGGCTAATCAACAGCATATCAAT 1528

QY 302 TyrLeuGlyAspLeuMetLeuAlaLeuSerPheSerLeuProCysGlyIleSerSerPro 321
 Db 1529 TACTTTGGGATGGCTGATTCATTAAAGTTGGTGTGGCCACCTGGTTCCAAACTCCC 1589

QY 322 IleProTyrPheTyrProIleTyrLeuLeuLeuIleTrpArgGluArgThrAsp 341
 Db 1589 TTGACATATTACTACTCTGTTTACTTCGCCAGCGTGTATTATACCGTCACAAACGAT 1648

QY 342 GluAlaArgCysAlaGluLysTyrArgGluIleTrpAlaGluTyrArgLysLeuValPro 361
 Db 1649 GAGCACAAAGTGGCGCTGAAATATGCGAAATTTGGGAAGATACGAAAGAAAGTTCT 1708

QY 362 TrpArgIleLeuProTyrValTyr 369
 Db 1709 TACAAGATCATTCATATGTTTAT 1732

RESULT 15
 AAT30357
 ID AAT30357 standard; DNA; 2528 BP.
 AC AAT30357;
 XX 25-MAR-2003 (revised)
 DT 21-NOV-1996 (first entry)
 XX Saccharomyces cerevisiae sterol delta-14 reductase gene.
 DE Sterol delta-14 reductase; ergosterol; biosynthetic pathway;
 KW identification; sterol biosynthesis; inhibitor; fungicide; ds.
 XX Saccharomyces cerevisiae.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 419..1735
 XX /*tag= a
 XX
 PN US5525496-A.
 XX
 XX 11-JUN-1996.
 XX
 PF 15-MAY-1995; 95US-00440674.
 XX
 XX 16-AUG-1993; 93US-00107347.
 XX
 XX (AMCY) AMERICAN CYANAMID CO.
 XX
 XX Bard M, Hsien-Pen Kuh Lai M, Kirsch DR;
 XX
 XX WPI; 1996-286399/29.
 DR P-PSDB; AAR98333.
 XX
 XX Saccharomyces cerevisiae sterol delta 14 reductase enzyme - useful in
 PT screening for fungicides for agricultural, medical and veterinary

PT applications.
 XX Claim 1; Col 13-18; 20pp; English.
 XX

CC The present sequence encodes *S. cerevisiae* sterol delta-14 reductase, a
 CC member of the ergosterol biosynthetic pathway, which is useful in
 CC devising screening tests to identify sterol biosynthesis inhibitors. The
 CC inhibitors are potential fungicides which may be used in various
 CC agricultural, medical and veterinary applications. The gene was isolated
 CC and cloned by selecting strains, carrying sequences on a 2mu based
 CC vector, for resistance to a morpholine fungicide, e.g. fenpropimorph.
 CC (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 2528 BP; 700 A; 469 C; 507 G; 852 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 5,17e-48 Length: 2528
 Score: 547.50 Matches: 133
 Percent Similarity: 53.87% Conservative: 76
 Best Local Similarity: 34.28% Mismatches: 136
 Query Match: 27.86% Indels: 43
 DB: 2 Gaps: 11

US-10-069-427-8 (1-369) x AAT30357 (1-2528)

QY 19 TrpAsnSerVal---ProLeu-----LeuValGly----- 27
 Db 587 TGGACCGTATCAAGCCATTTCGCTACTATCTGGCAATCGTGAATTATGGAGCTGTAT 646

QY 28 -----PhePheThrTyrLeuAlaValAlaGlySerIleLeuProGlyLysLeuValPro 45
 Db 647 TGCCTGTGGTATGGAACTGTCGAGCTTTTGGACGTCATTTTACCGGCGAGTCATGAAG 706

QY 46 GlyValAlaLeuLeuAspGlyThrArgLeuHisTyrCysCysAsnGlyLeuLeuSerLeu 65
 Db 707 GGTGTTTCAGTTAAGGATGTTTGAAGCTTTCGTATAAGATCAATGGAATTGCCATGCT 766

QY 66 LeuLeuLeuValAlaLeuLeuGlyIleGlyAlaLys----- 77
 Db 767 ACAACTTTGGTCTTAGTTTGGCTATCAGATGGAATTCAGTATGGACAAATTCGCTGAA 826

QY 78 MetGlyPheValSerProThrAlaIleSerAspArgGlyLeuGluLeuLeuSerThrThr 97
 Db 827 TTGCAATATCTGTATGAATAATCAGTTAGT-----TTATGCATATATATCTATT 877

QY 98 PheAlaPheSerPheLeuValThr-----LeuLeuLeu 108
 Db 878 TTTTCGTTTC---TTTTGGCGAGCTACTGCTATGTTGCCAGCTTCATACCATTTGATCTTC 934

QY 109 HisPheSerGlyCysLysSerGlnSerLysGlySerSerLeuLysProHisLeuSerGly 128
 Db 935 AAGAAAAATGGTAAATGCGCAAAAGGAAAGATCTTAGCACTAGGTGGAAT---TCAGGA 991

QY 129 AsnLeuIleHisAspTrpTrpPheGlyIleGlnLeuAsnProGlnPheMetGlyIleAsp 148
 Db 992 AACATCATTTACGATTTGTTTATTGTTAGAGAACTGAACCTCGTCTCGGCCCATAGAT 1051

QY 149 LeuLys-----AlaGlyMetMetGlyTrpLeuLeuIleAsnLeuSer 162
 Db 1052 ATCAAGATGTTTTCAGAGTTTGAGACCCCGCATGTTTATGGTTACTGATCAATCTTTC 1111

QY 163 IleLeuMetLysSer---IleGlnAspGlyThrLeuSerGlnSerMetIleLeuTyrGln 181
 Db 1112 TGTCTGCATCCACATTACTTACAGAGCTGTAATAATCAACGATCGATGGCTTGGTTAAT 1171

QY 182 LeuPheCysAlaLeuTyrIleLeuAspTyrPheValHisGluGluTyrMetThrSerThr 201
 Db 1172 TTCGCAAGGATTTTACATTTTCGATCGAGTACTAAACGAGGAGGTGATTAAACCATG 1231

QY 202 TrpAspIleIleAlaGluArgLeuGlyPheMetLeuValPheGlyAspLeuValTrpIle 221
 Db 1232 ATGGATATCACTACAGATGGTTTGGTTTTCATGCTAGCGTTTGGTACTTAAGTTAGTT 1291

